

AAAAAGAACT ATTTGCAGAA AA

202

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SEQ ID NO:7204

SEQUENCE LENGTH:337

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08443

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SEQUENCE DESCRIPTION:

GATCGGAAAA CTCTGATTGA ACCATTCACT TTATTAGCCA GTAAACTTTC TCAACCCAG 60

AGCAAATCAA GCTTTCCTTT GCCTGGGAGG AAAANCATAG GGAACCTCTAA TTCTGAGAAC 120

TAAAAATCAG TAATTTCCAC AATTGTATGT TGAATAGTGA TTGCCTTTAN GNGNCTGTGN 180

15

NCATGGAGTA ATATTACTAT TTAATAATAGG CCATTGTAT CTACCTTTGG TCCTTAGGAA 240

AATTCCTAAG GAAGTCAATT AATGCACITT NAGATGTTAA AAGTATTTGG GCTAAGGTTA 300

TTATTGCCTG ATATGGAAAT AATTATNNTT CTGNTTN 337

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SEQ ID NO:7205

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08444

25

SEQUENCE DESCRIPTION:

GATCAGTGAC AATTACAGG AATGTAGCAG CGATGGAATT CCCTGGAACA GTTTTTTGTT 60

TTTNTTTTTG TTTTGTGTTT TGTGGGGGGG GGCAACTAAA CAAACACAAA GTATTCTGTG 120

TCAGGTATTG GGCTGGACAG GGAAGTTGTG TGTGGGGGTG GTTTTTTCT CTATTTTTTT 180

GTTTGTGTTCT TGTGTTTNA TAATGTTTAC AATCTGCCTC AATCACTTTG TCTTTTANAA 240

30

NGNTTCCACC TCCAGTCCTN TCTCCTCCCC CTTACTCAGG CCCTTGAGGC TATAGGGGGT 300

TNCTTNGAGG ACCTCANCAA AATCCCAATC CAAGTNAACC TTTTGCACAN N 351

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SEQ ID NO:7206

SEQUENCE LENGTH:273

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08445

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SEQUENCE DESCRIPTION:

GATCTATTTC TTTAAAGAT ATTTGTGCAG AACTGCATG TAACTCTAAG TTTTACTCCT 60

AACATACATA TGTTTGGGGA AGTATTCTAT TCTATACTTG CCAATGTGGA GAACAAAATA 120

GTTTTTTTAA GAATGAAGAA GTATATATAT CCATTCTGTA TTTTACGTGC AGCAGAATTA 180

TCTTCCGTAG GATTTTTTTG TGTATTACACA AGGTGATATT TGTATTGTAA AACAATAATG 240

45

GTGAAGGAAA TAAAAAGGCT TTTAAATTT AAA 273

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SEQ ID NO:7207

SEQUENCE LENGTH:328

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08446

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SEQUENCE DESCRIPTION:

GATCAGATTT TTAATAAATG GATTTCAT ATAAATAATA TTATCAAAA AGGATTCTC 60
 ATATAAATAA TATTATCAA AAAGCTGATT TAAAAGTTT CTCCCAAAGT CTTATTCTAG 120
 TAATTATAGA GACCTAGGTA ATGAGTGGCA GATATATCTG CCTTTCAGAT ATGCCGTAAT 180
 GTGAAAAATA ACACAGTCAT GTGATATTCT TNATTAATA AACTGTGTT GTTTTATTT 240
 TGGAGTAGTT CTCATAATTC ATTGGTAGGG AACTATCCAG TATTATATT CCTATGTATG 300
 TNTATCAGNT TAATTTTGAG GCTTGGAN 328

SEQ ID NO:7208

SEQUENCE LENGTH:145

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08447

SEQUENCE DESCRIPTION:

GATCTGTACA TACAGTGTTA AGAATGTAGA TATTAATTTA GCTGTACAT 60
 AATATTAAGA CTCAGAGTTA AGTAATTCA CTGAAATTGA TTGCTTTTG TGTCTGGAG 120
 TCAAAATAAA TAACTGAAAT CTAAT 145

SEQ ID NO:7209

SEQUENCE LENGTH:227

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08448

SEQUENCE DESCRIPTION:

GATCTGTNA CATAAGCACT AGTCACAGGA CTAAGTGA ATTCATCAA TTTATTCTAT 60
 TGTGTTTATT CATGATATCA CCTTAGTAAT TTTGAAAAA AAAAANGTAC CACTTGGC 120
 CAAANGCTCA TCAGGCTGAT TGTTTANCTG TNGCTGATTG CTTATCTTTA TATTGTATGA 180
 CCCNGGGGNT NGNTTTGAAN GTTATATTAG GTTTGAAATG ANTTATN 227

SEQ ID NO:7210

SEQUENCE LENGTH:333

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08449

SEQUENCE DESCRIPTION:

GATCTTTGAA CTCTGCAATA TGAAGCATAT ATGTGAGTGC TTAGCTTTCA CTCTCTTTCT 60
 GTGTGTGTGT GTGTGTATAC AGATACTAAG ACACAGATAC ATTCACATAT ATACATCTAA 120
 ATATATATAC AGTACAGTCC ATATTCAGAT TTCTTCAAGG TTATGGGTCT ATTGTTTAA 180
 TTCGGAATCC AGTCAAGGAC AACACATTAA AATTGATTGT TTGCCTCTA CAGTGTGTT 240
 TTTTGGTTTT CATGACATTG ACTTTGATT GAATAGGTCA GACCATTTCA TGTACTTTAT 300
 ANAGGCATT TGTAGATTG TCTGATGATT TGN 333

SEQ ID NO:7211

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid

EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS08450

SEQUENCE DESCRIPTION:

5 GATCAAGAGA GTTCGATTGG CCAAAGAACA GGAATCCCGG GCAGATTGTA TCAGTGAGTT 60
TATAGAATGG CAGTATAATG ACAATAACAC TTCTCATTGT TTTAACAAAA TGACCAATCT 120
GAAATTAGAG GATGCAAGGA GAGAAAAGAA A 151

SEQ ID NO:7212

10 SEQUENCE LENGTH:275

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08451

15 SEQUENCE DESCRIPTION:

GATCTGACAG ACGTCAATAC CTGCAGGCGT CTACAGAGAG GAAATTTGAT AAAAATATTT 60
TAGTCACTGA CTACACTACC ATTATCTGAA GCATTCAGAT AAGACTTAGC AGAGAATGTC 120
AGATTTTGT TTCAATTATA ATTTTAGAAA TGCAAAATCT TATTTTTTCT AAGTTGCTTA 180
TTGTCTATAT AAATGTTTTA TATCATTTAA AAACATGCAG AATAATACAC CTGCAGAATA 240
20 AAAGAGCTGA AATTAAAATA TCTTTTTCAA TNAAA 275

SEQ ID NO:7213

SEQUENCE LENGTH:103

25 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08452

SEQUENCE DESCRIPTION:

GATCACTTGA GTCCAGGAGT TTGGTGTTAC AGTGAGCTAT GATGGCACCA CTGCACTCCA 60
30 GCCTGGGCCA CAGAGTAAGA ACATGTCTTT AAGAAAAAAA AAN 103

SEQ ID NO:7214

SEQUENCE LENGTH:144

35 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08453

SEQUENCE DESCRIPTION:

GATCTGTAGA CATGAAGGCA AAGCTCTTGT ATTTTTTTTT CATCCAAACA CCTCAATTTA 60
40 TTTTATAAAT TCGTTCATTT TTCCTGTTAT GTTTTATATA ATATATGGAC TAAACAAAAT 120
AAAATAACAG TGCAAAAGAG GAAA 144

SEQ ID NO:7215

SEQUENCE LENGTH:164

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08454

SEQUENCE DESCRIPTION:

50 GATCAGAAGA GGATGACAAT GGCAACAAGT GTTTGGAAGT TCCAAGGTGT GTTCAAAGAG 60

55

GCTTGCCCTTG AGGGAGGGCT GGAATCTGTC TTCCCTGACT CGGCTCCTCA GGTCTTTAGC 120
CTCCACCTTG TCTAAGCTTT GGTCTATAAA GTGCGCTACA GAAA 164

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SEQ ID NO:7216
SEQUENCE LENGTH:332
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

10

CLONE:HUMGS08455
SEQUENCE DESCRIPTION:

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GATCTGAAGT CCCCCCAACC CTCTCCAAGT AAAGTAGTTT ATTAGAAGCT CTTAAGTCTT 60
TAATAGACCT GCATATTTCC TTCCCTTATG ATTTCCTATA AAATATAGTT TATGGTGTTA 120
TATTTTAAAC TGAATACTG TACATATGTA AATAACTCTT GACAGGAAGA AAATATATTA 180
ATGTAGTATT TGCCCCCTAT CAGTGAGCTG AACAAATACA TCATTTAAAT CTATGCTGCA 240
CTTTGAGTTG CTACAAATAT GGTTCGNTTT GTTTATTTT GAAAAATGTG ATAAAGAAAT 300
CTAAAGANTG NNNNAANTAA NNNNNNNNG NN 332

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SEQ ID NO:7217
SEQUENCE LENGTH:277
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

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CLONE:HUMGS08456
SEQUENCE DESCRIPTION:

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GATCTGTACC ATCCTGTTGC TGCTGTATGC GTTCCATTGA TGGGACATCT TCAGGGACTC 60
TTGACAGCCA CCGCTTTCAC ACCCTGGTCT GGAATAAGGA AACATCGGAG GGAGAAGTTG 120
ACTGTCTTGA TAATTAGCCT GACCAGCAGG ATGAATGCAA GACTGACAGT GATGGACTCT 180
GTGACATGGT CAGGTTGAGC TGAAGCCACA GTTCTCTGT GCTGTGTTTT CTAACACATT 240
TTTCTGTTTT TAATTAAGAA AANNNNNNNA GGGTAAA 277

35

SEQ ID NO:7218
SEQUENCE LENGTH:198
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

40

CLONE:HUMGS08457

SEQUENCE DESCRIPTION:

GATCTTAAAC TCCTGACCTC AAGCAGTCTA CCCCCGTTGG CCTCCCAAAG TGCTGGGATT 60
ACAGGTGTGA GCCACTGCAC CCAGCCAAGT TTATGTATTT TNATTCTTTT TCATGAATGT 120
GATTTGTAA ATNAGTGATT AAATATAATT TTNATATATT TGTATGACTT TNCTGTAAAT 180
AAAATTTAAA ATCAGAAA 198

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SEQ ID NO:7219
SEQUENCE LENGTH:409
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

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CLONE:HUMGS08458

SEQUENCE DESCRIPTION:

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EP 0 679 716 A1

5 GATCTGCATC TNACGCCAC TGCACACCGT TCCTCTCCAT CTGCCCTTCC CTCCCAGGCC 60
 CCCGGTCGGG GGAGCAGGTG TGGCAAGTGT TAGGAACTCC CTTCTGGTGA CAGCTGGTCT 120
 TCCTAGAGTG TTGCTGGTAA CTATCGCCTC TTGGTCTTCT GACATCATTG CCAGGAACGG 180
 GGCACTTTTT CGTCTTGTAG TTTGGCCCTC GGGTTTCCTC ACTAGGTATT GTGTAACTCC 240
 CTCAAAAAAA GGTTTATGAA ATGCTGAACC TCAGGTTTCA TAGACGTCTT TGTACACTAA 300
 AAATTCTGCA GCAGGAATAT TTTTAAACAT TCGCAGTTTT TTGTAAGCTA TATTTTTTGG 360
 ATATTAAAT TGCTATNTNA AAANTTTTAA ANTNNATTTT GCTAATNNN 409

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SEQ ID NO:7220
 SEQUENCE LENGTH:87
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

15

CLONE:HUMGS08459
 SEQUENCE DESCRIPTION:
 GATCTCCTGT TCCGTTAGAA ATACGGTTAT GTTGACATTA TGGTTACTGT GCTTGTGGTT 60
 TTGCAATAAA CATGTATTGA AAGCAAA 87

20

SEQ ID NO:7221
 SEQUENCE LENGTH:130
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

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CLONE:HUMGS08460
 SEQUENCE DESCRIPTION:
 GATCAGATAA AATAACTCCT GACAGAACT GTNNGGAAAC CAGCTGAATG TTTGACCTGA 60
 TGACTGATGT TGTATGGTTT ATGTTAAATG TATATTCTTT TAATCAATGA ATAAAGCATT 120
 AAAAATGAAA 130

30

SEQ ID NO:7222
 SEQUENCE LENGTH:251
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

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CLONE:HUMGS08461
 SEQUENCE DESCRIPTION:
 GATCAGAAAC ATTTACAATC TATTCTCTTT GAAGCCTGGC ACCTGGAGGC GTCATCTGTA 60
 TGAGANNNNN GGACTCCACA ACCTTTTATC ATAACCCAGA CATTCTTTTC TATTGATAAT 120
 AACCAATTGC CAATCAGAAA AATTAATAAT CTACTTATAA CCCAGAAGCA CTACCCCGCA 180
 ACCCTTGCTT GCTTCAAATT GTTCCAACCT TCTGGACCGA ACCAATGTAT AGCTTAAATG 240
 TATTTGATTG N 251

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SEQ ID NO:7223
 SEQUENCE LENGTH:189
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

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CLONE:HUMGS08462
 SEQUENCE DESCRIPTION:

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EP 0 679 716 A1

5 GATCGGTGCC ATGGCAAGCA CACCCTCAGT CATCATCCTC ATCAGGACAG NCAGCCNNGA 60
 ACTCAAGTCT TACGCTTTGG GAGTTCTTTT TCTCNTCCTT CGTTTGTGG GCTTCATCCC 120
 NCCACCCCTC ATCTTCGGGG CTGGCATCGA CTCCACCTGC CTGTTCTGGA GCACGNNNTG 180
 TGGGNGAGN 189

10 SEQ ID NO:7224
 SEQUENCE LENGTH:97
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08463
 SEQUENCE DESCRIPTION:
 15 GATCTGATTT GGCCTGGGAC CAGTGTTCAA GTTGGTTTGG TCTTTATTAA AAATCACAAT 60
 ATTCCGAAAA CAAAAAACC TAGGAGATAA ATGTAAA 97

20 SEQ ID NO:7225
 SEQUENCE LENGTH:255
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08464
 SEQUENCE DESCRIPTION:
 25 GATCTGAAAT NAGAGGTTTT GGTTTACCCT ATCTATGGTA TGTCTTAAAA ATCAACGAAG 60
 ATGTCCTTGT CTTTTTTNAA TTNCCGAGT GTGTTGCAGT TCCACAGCTC ACTGTTAGGT 120
 GGCACATACC CCAAAGTAA AACCTGACCT CGTAGGGCAT GAGTCAAAAG ACAGGTAGGC 180
 ACAGGACAGG GCAGTGTGA CACTACAGCT TTCAGGGTTC CCAGCCTGTC AAGAATGAGC 240
 ATGTCTTAGC AGGGN 255

30 SEQ ID NO:7226
 SEQUENCE LENGTH:63
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 35 CLONE:HUMGS08465
 SEQUENCE DESCRIPTION:
 GATCAAAATT GGAACCTA ACATTGAGAC AATACTATAT TAAAGTATCT CTGGTACCCG 60
 AAA 63

40 SEQ ID NO:7227
 SEQUENCE LENGTH:55
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 45 CLONE:HUMGS08466
 SEQUENCE DESCRIPTION:
 GATCCAGCAA TCTCACTGAG TATCTAACCA AAGGAAAATA AATCACTATA CCAAA 55

50 SEQ ID NO:7228
 SEQUENCE LENGTH:220

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08467

SEQUENCE DESCRIPTION:

GATCCAAGAA CCCTCTCTTG GGGTCTGAAT CATACCCCTT TCGGGTTACA GCCTATCACA 60
GCATTTTAA TCCTATGCAC TTAACACTTC TGTATAGAAA AAGAACATCA CACTAGAATT 120
TTGATGACAA TAGATGACAA TATGATGAAT NTTATTATAT GAAGTGTTAA ACTTATTAGA 180
GCAGATATGG TACTAAAAAT AAAATCCCAC CTNCNCTAAA 220

SEQ ID NO:7229

SEQUENCE LENGTH:114

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08468

SEQUENCE DESCRIPTION:

GATCGCGCCA TTCCACTCCA GCCTACACGA CAGAGTGAGA CTCCATCTCG AAACAAAAAA 60
AAGACTTGAT TTTATTTTC ACTATCTTTA GCATAAATTG TTCTAAGAGT GAAA 114

SEQ ID NO:7230

SEQUENCE LENGTH:274

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08469

SEQUENCE DESCRIPTION:

GATCTTATAC AGAGAAGTAT TTTATTAATAA ATTCAAAAGG GAAGACTTTT ATGTGCTCAT 60
TTTGTAATTT TTAATTTTAA ATATCTTTAC ATTGTCTGCC AATTAAAGTG TTTTAACTT 120
GCATTGGAAT GGNCTCTGAA TGTATTTNTN TGGTGTNACG TTATCCGTAG ATTTCTAGCA 180
TGANGTAGC CTCACGATGC TGTGCAAAGG ATTTTNAAT ATGAGAGTCA CTGANAGAGT 240
TTAANCATCT GTCCATGTTA AATGCTCTAT GGGN 274

SEQ ID NO:7231

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08470

SEQUENCE DESCRIPTION:

GATCCTTTGT TCACGGCTCT CCTTAATGAC TGAGTGAACA GTTCCTATCT GTATATTTGA 60
CTAAACCTTT TCCTAAGCTA TCTCTCATGG TTCCTATGTT TTTTATCAT AATTAAAAAGC 120
AAAACCATCT GAAA 135

SEQ ID NO:7232

SEQUENCE LENGTH:238

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08471

EP 0 679 716 A1

SEQUENCE DESCRIPTION:

GATCGAGCGG AAAATTCCAG AACTGTACAA GCCAATATTC AGAGTTGAGA GTCAAAAGAG 60
 AACATTGTGC TGTCTGTCAG CATATGTATA TCAGCTACAA AATATATTCA ACTTTGACTT 120
 CTTTGTACAA AGGACTTTAG GAAAAAGAGG AACAAAGACA TTATTGAGA ATTAAATTAT 180
 ATATTTTAAN TATGACTGTG ACCTTGACTG ATAATAAAGA TGTAATAAGA NTTGCAAA 238

SEQ ID NO:7233

SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08472

SEQUENCE DESCRIPTION:

GATCAGTTCA GCCAAGCAAC TGACAAATCA AAAACCCACT TGTGAGTTTC GTAAAATAAT 60
 TTGGTCAGAA A 71

SEQ ID NO:7234

SEQUENCE LENGTH:347

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08473

SEQUENCE DESCRIPTION:

GATCTAGAGG GCTTCGAGTG AAGCCAATCA TGTTGAACGA AACTGGGTC AGTGTAGATG 60
 AANTAGAGTG AGGCGTATGC AGTCATAAAA TGAAGGGTGG ACAGGAGATT ACATTGGAAG 120
 AAAGGATAAG CACTCAGACT TGGTCTCTTT TAAATTAATA TATTTCTTTT CTCATGTGCA 180
 AATGTATATC AAAGACTTGA ACAGGTATTC TCTTGAAATT TGAGGATTTT TAGTTTTTAA 240
 TGCTGNCCTT GCTTANNATT AANNATGNGT NGCCTATTGG TTCCCAAATT GTNTGGGGNC 300
 CCTAANNNGT NCCCTNGAG GGGTNCATTT TTGAAGGNGG GTTANGN 347

SEQ ID NO:7235

SEQUENCE LENGTH:93

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08474

SEQUENCE DESCRIPTION:

GATCTTGTGT TTGCTATCC TTTTACTGT AAAATGTAAA TATTTTAAGG GATATTTTGA 60
 TTCTAAATAT GATAAAATAA TTTCTCACCT AAA 93

SEQ ID NO:7236

SEQUENCE LENGTH:417

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08475

SEQUENCE DESCRIPTION:

GATCCCAATT CAACTTATCC AGAATAATTC TCTCCATTCT CAAAATTCA NATGAGGAAC 60
 ATNNNNAGAA ACTGTCTCTT GCCAATACCT TTAGTACTGG AATTCTCTCA TCTTCCTCAA 120

CAGTCTTGGC AGCTAGGAAA AAACAGCTGA TTGCAATACA ACTCAAGTAT TTTGGATGAG 180
 CCTTTACGGT AGCTAAAAAC CCATCCAAAA GACTGCTAGC CAGAGCAAAT GTTCTGGGT 240
 AAAGGTTGAA TTGGTACTTG AGTTTGGCCA GCCATTGANT TACTTCATCT CTCTGGGATG 300
 5 GNGAACATTC TGATTGAAG GCATTTCCG CACATTCATC TTCCACATCT GTGNCTCCCT 360
 AGTGATTGCC TTTTCCACCA GGAANGCCAA TCTCTGGTTT TCCAAAGGCC CTNGGAN 417

SEQ ID NO:7237

SEQUENCE LENGTH:80

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08476

SEQUENCE DESCRIPTION:

15 GATCAGACCC TCCTGTGGGC AGGGTCTTA GTGGATGAGT TACTGGGAAG AATCAGAGAT 60
 AAAAACCAAC CCAATCAAA 80

SEQ ID NO:7238

SEQUENCE LENGTH:409

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08477

SEQUENCE DESCRIPTION:

25 GATCTGCCTG CCTCGCCTC CCAAAGTGCT GGGATTACAG GCGTGAGCAT TTGCGCCTGG 60
 CCAGAAAAAT ACCTTTAAAA AGCTGGGCCT GTTGGTGTAC CTAAAGGATA ATACAGATGT 120
 TCCTCTCAAC TTAGCATGGG GGTGTGTCT CAATAAACCC ATTTTAAAGT TGAAANGCCTT 180
 ATGTGGAAAA TGCATTTTAT TATACCTAAC CTACTAGACC TCGTAGTTTA GCCTCCCTTA 240
 CCCTACAGGT GCTCAGAAC CTTTNGNAGG CCCTACAGTT NGGGCAGTCA TCTAACACAA 300
 30 AACCTATTTT ATAGGTAAAA GTNGTTTGAA TATCTCAAAG NTAATTTATT TGAATGGTTN 360
 CCACTTGAAT NGCGGANTCN ANGTTGTTNN NAACCNGTNT GGTNNANN 409

SEQ ID NO:7239

SEQUENCE LENGTH:123

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08478

SEQUENCE DESCRIPTION:

40 GATCTCATAG ACTTAGTACA AAAAAAGGTG AAATGTCTTG ATATTTTGT ATATTGATTA 60
 TTGAAATAAC CTTTATGTT GGGCTAAATA CAAATATGTT ATTAATAATNA ATTTAACAAC 120
 AAA 123

SEQ ID NO:7240

SEQUENCE LENGTH:265

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08479

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCTGAGGG GGAGAGGGGAC GGGTCGGGCC AGCTGGTCAG GAAGGGCCTT GAGGGCCTGC 60
 AGCCAAGAGT AGCAGTTTTT TCCCCCGTCT TGTTGTTCTT GGTCCCTGGA CCACAGGGCA 120
 CACAGGCCGTG GACACCATAA GGCTGGTGGG CTTTCAGAAT TGTGTTAGGG NNNNNAGT 180
 GGCAGGTTCC TGAATCTCGG TCAATATAGT AACCAGCAGG ACAAGAGGTT CAGGAGGAGC 240
 CCACATCAGA GGCTTCTAGG GCAAN 265

SEQ ID NO:7241

SEQUENCE LENGTH:265

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08480

SEQUENCE DESCRIPTION:

GATCTCTTGA ATTGCCATCT GTCATCTAAG TCTAAGGCTT TATGCTTAAT GANTTGTGGT 60
 GTACTAGCTG GACTAGCTTC AGGAATGTCA GTGTGTTCTA CCATTAAGGT CAGATTGTCT 120
 ACTACATCGA GATGGTGGTT GTAGTTACAG CTACTTTTAG AAACATGTCT ATTTTTTAAA 180
 GACATAACAC ATGAATGAAG AAATTCAGAA TTTGGAAAAA AGGTCGGTAA TGCCTGACAA 240
 AGAAAAATGT TCTCCTGAGG GTCTN 265

SEQ ID NO:7242

SEQUENCE LENGTH:138

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08481

SEQUENCE DESCRIPTION:

GATCCCAGCA CCTTCACATC TTCAGCAACC CAGNNGNTCA AATTTGACCT GGTGTTATTT 60
 TAGCCCCAAA TTTATGACAT TACACAATAT TAAAATGTAA ATGTTTCTTC ACCCAAACCTA 120
 CTTCTAGATA TNCTNGNN 138

SEQ ID NO:7243

SEQUENCE LENGTH:273

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08482

SEQUENCE DESCRIPTION:

GATCCTTTGA GAGATGGTTT GACTTTCCCC GAGCAAAGAG CCTGCGTTGA AAAGCGGGGG 60
 TGGAATTCAG TCCTCACAGA TAATGAGGGG ACAANACCTA ATTGANCCGN GTATTGCCGG 120
 GAAGGAAAAG GCAACGGGCC AAGCCTTTGA CAGGGTGCGA AACTGACTTT NATCATCGTT 180
 ATAGTCTTTA AATCCTGGGA AACGAGTTGG CAACCCCAA ATAAAGAAGT GTAATGACGT 240
 CTGATGACTT CACCCAAATA CAGACCATTC CAN 273

SEQ ID NO:7244

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08483

EP 0 679 716 A1

SEQUENCE DESCRIPTION:

GATCTATAAA ACAGACAGAG ATAAGTACAA CAGAATATCT CGGGAATGGA CTCAGAAGTA 60
TGCCATGTGA TGCTACCTTA AAGTCAGAAT AACCTGCATT ATAGCTGGAA TAAACTTTAA 120
ATTACTGTTA AA 132

SEQ ID NO:7245

SEQUENCE LENGTH:321

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08484

SEQUENCE DESCRIPTION:

GATCCGCCTG CTTCAGCCTC CCAAAGTGCT GGGATTAGAG GCGTGAGCAT TCATGTCCAG 60
CCAGCACTGT GCTGTTTTG ACATGCATGT TCTCATTAN TGCCATGCGG CAGATTCTAG 120
GATTATNATT ATNCTCACTT TACAGATGAG GGAGTGAGAC TTAAAGGGGT TAGGTAATTT 180
GCCACATCC CCAACTAGC AAATGGTAGA GCCAGGATTG GAATTTGTTC AGGCTCTTAA 240
CCATTGCACT CTTTCAAAAT GTTAAAAATA ATGTTGTGTC TCATTTTAAA AAATTAATA 300
AAANCTCTTT GGACCAAGAA A 321

SEQ ID NO:7246

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08485

SEQUENCE DESCRIPTION:

GATCTCCCCA TTTGGAGACA GAGCCATTG GATATTTNCC CCTTNAACTT CTCCANNNCC 60
TGAAGCGTTC CTTCCCTGGA GGAACCTTTT GGTTCAGGG CTAAACTN 108

SEQ ID NO:7247

SEQUENCE LENGTH:139

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08486

SEQUENCE DESCRIPTION:

GATCTCAGCT CAAATATTCC TTATGCAGAG ATGCCTTCCC CTGATTCCCT AAAC TAGACT 60
CGGACCCCTC TGTCTGCAT CTCTGTGGCA TATCATCTGC CCCTTTTGTAA AAAC TTATAA 120
ACTTGTGGTT ACTTGTA 139

SEQ ID NO:7248

SEQUENCE LENGTH:244

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08487

SEQUENCE DESCRIPTION:

GATCATGTGA GCTCAGGAGT TCGAGACCAG CCTGGGCAAC ACAGCAAGAC CCTGTCTCTA 60
TTTTATTCTA TGTTTTAAAA TTTAAAAATT AAAAAGAAAA AAGAATAACA TTTTATAAGA 120

EP 0 679 716 A1

AAATATTTTA TGAGAGACTT ATAAAAGAGA CATTAGAAT ATGAAGTAAT ATATTNCGTA 180
TTCCTTATCT CAATAATGCT GTAGGGAAAA ANCAATTGAA ATAAAAGCAG TAAATGAGTG 240
GAAA 244

5

SEQ ID NO:7249
SEQUENCE LENGTH:155
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08488
SEQUENCE DESCRIPTION:
GATCTAACTT GCAGTGTATT TTCTAGGCTG GAAAGTGGAA AATNAAATAT ATTATAATCT 60
TAGGTTACAT AAAGTTTCTA AAGTTTCAAA GAGTCTTGAT ACAAAATCAG TTTATATTCT 120
GAAAATATTT ATAATAAAGT ATTCTAATTT CTAAA 155

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SEQ ID NO:7250
SEQUENCE LENGTH:96
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08489
SEQUENCE DESCRIPTION:
GATCGCACTG GAAGATTTTA TAAAAGAATT TTTGTGGGTC GGGGGGACAG TAAACTTCCT 60
GGGCCACGTG GGTCTTCAG GAGTTTTTCA GGCAAA 96

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SEQ ID NO:7251
SEQUENCE LENGTH:118
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08490
SEQUENCE DESCRIPTION:
GATCTNATAT TGAACCTAT GCCAAATAGC GTGGCATGAG GCCAGAGAAC AGTGCTTNCC 60
TTCCCCGNCT CCACCCAAAT TGTCCTTGC TCTNGATATT ATGCCAGTNC CATATTTN 118

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SEQ ID NO:7252
SEQUENCE LENGTH:391
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08491
SEQUENCE DESCRIPTION:
GATCTGGAAT CTATTGGNT TTTNTTTTCA ACTTTTCATT TGGATGTTTG GCGTTGCACA 60
CACACATCCA CCGGTGGAAG AGACGCCCGG TGAAAACACC TGTTTGCTTT CTAAGCCAGT 120
GAGGTGAGG TGAGAGGTTT GCCAGAGTTT GTNTACCTCT GGGTATCCCT TTGTNTGGGA 180
TAAAAAAAT CAAACCAGAA GCGGGGATGG AATGGATGCA CCGCAAATAA TGCATTTCCCT 240
GAGTTTNCCT GTTAAAAAA ANTTTTTTTA AGTAAGAAAA AAAAAAGGTAA TANCATGGCC 300
AATTTGTTAC ATAAAAATGNC TTTCTGTGTA TANNITATTC CTAAAAATC CTGTTTATAT 360
AANNNTTCAG TAGNTGGAGA AACTTTCCAT N 391

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SEQ ID NO:7253

SEQUENCE LENGTH:385

SEQUENCE TYPE:nucleic acid

5 TOPOLOGY:linear

CLONE:HUMGS08492

SEQUENCE DESCRIPTION:

GATCATGAAT CTCTAATAAA TTAAATCTC TTAAACCAGT AGGTGCTTAA TATTTTTTAA 60
 TTTGATTAAT GCCCATTTAA ATCTCATGGG TTCTATTAAA AATATATATA TATAGGGCCC 120
 10 CAATCCATTG CCATCAAATT GCCCTTGGAC TTTTCCAAGG TATATTATGG GGTTTTATGC 180
 AAAATTCCAA GCTACCATGT AACTTTTTTN AACCATTTAA CAAGGAGGGG GAACTGTTTC 240
 CTACCTTCTT TACATGTTGT GCATTGTTGT GGTCCAGAAA TGCCAAACCT TTTTAAAGAT 300
 GGTGCAACTT TGAGTCCTTG GCTTGACTAT ACAGGNCTTG AACTTCATGG CATATCAACT 360
 15 TTGNCATATC TGCAGGTGNG CTGTN 385

SEQ ID NO:7254

SEQUENCE LENGTH:414

SEQUENCE TYPE:nucleic acid

20 TOPOLOGY:linear

CLONE:HUMGS08493

SEQUENCE DESCRIPTION:

GATCACCATT TTTTCCAGG CTTTCTGCCT CCNAGATGTG GCACCATAGT GCGGTGCCCT 60
 25 GTGGCTTAC CGCCCTACTT CCACCTCCGC CCAGCCTGTA ATGTTTATAT AAGCAGCCTC 120
 AAGGACCAAG AACCATCTGC GAAAGGACAC ACACAGGAAA TTCATAAAAG AAATCTGANT 180
 GGNTAAAACC ATGAAAAAAA GTATGCTTCA TTAGTAATTA AAGAAAGGCA AATAGAGCTG 240
 GAAGCNTTTT NCCNTTNGCA AACCATAACA GAAAANNNTA NGACCCAATA TTGGCAAAGA 300
 GACTACTGAA AANCCATTCC CATACTTGC GTGTGGGNGT ATACATCGGT GCAGGCTTCC 360
 30 TGGATGACAG TTGGGTGATA TGTGTCATGT GGCCTAANAG CCTCCATGTC ANTN 414

SEQ ID NO:7255

SEQUENCE LENGTH:207

SEQUENCE TYPE:nucleic acid

35 TOPOLOGY:linear

CLONE:HUMGS08494

SEQUENCE DESCRIPTION:

GATCCTGGTT TTGTGATTGA CAATATTTCA TGCTCTGTAG TGAGAGGAGA TTTCCGAAAC 60
 40 TCTGTTGCTA GTTCATTCTG CAGCAAATAA TTATNATGTC TGATGTTGAC TCATTGCAGT 120
 TTAACATTT CTNCTTGTTC GCATCTTAGT AGAAATGGAA AATAACCACT CCTGGTCGTC 180
 TTTTCATAAA TTTNCATATT TTTGAAA 207

SEQ ID NO:7256

SEQUENCE LENGTH:412

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS08495

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SEQUENCE DESCRIPTION:

5 GATCAAGAGT ACACTTCCTG GCAGTGATTA AGGAGTGTGT ATCTAACAGA AAAAAATATAT 60
 ATACCCTGTG AACCCGAATA TGGAATTCAG ATTGTTTCTG CCCTCAGTAT CATACTTAAA 120
 AAACAAGCAT ACAAACAAAC ATAAGGGAAC AAACAGCAAC CATAACAAAA ACAAACCTTT 180
 AAAGGTGGGT TTTTGCTGTG ATAAATGAAT ACGGTACTCT GAAGGAGAAA AAAGTTTCTC 240
 AAATGAGCTT AAATGCAAG TGATTTAAAA NTTAGAGAAT ATAATTCTTA ANGCTATTGA 300
 AAGTTTCAAC CAGAAANCCT CANGTGAATT TTGTATGTAA ATGGCATCTT GNNTGTAAGT 360
 10 TCTGTGNTTC TTTAGGCAAC CAATTAGCTG GAACCTTGGT TTTGTGTGGT TN 412

SEQ ID NO:7257

SEQUENCE LENGTH:406

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS08496

SEQUENCE DESCRIPTION:

20 GATCTGCAAA TCAAGCTACA TGTATTTGTG TATAAGACCC TGTGTTCCAGG ACTGGGTGAC 60
 TTTTCTAAGA AATATGGGGT TTAGAATGGG GTTGACTGTA TTTNTAAACC TAATTCTGGA 120
 GAGAAGATTG TATTNTAAC AGTTTTTTGG GTTTGGCTTC CTTCTCACAT TTCTTTAGCT 180
 TTGAATTTTT ACTAAATAAA TTTCTCCTG ATTAATTTTT TTTTCCCCA TCTGGGAATT 240
 TGAAATCTCG GTGCTTACTG TNACACCAAT TTGTCCAANG GGTGAAATC ACTTTAATGC 300
 CAGACCATGG TAATTTGCAG CCATTTCCAGG CAGGTGGTGG NCCTTTTNA TACCATCGTT 360
 25 ACGGGGTCCC NTAAATATT CTGGGGGGTG ATGTAAATNT AACGGN 406

SEQ ID NO:7258

SEQUENCE LENGTH:116

SEQUENCE TYPE:nucleic acid

30 TOPOLOGY:linear

CLONE:HUMGS08497

SEQUENCE DESCRIPTION:

35 GATCTCCATT TCCGCCAGCT GCCTGTAGCC ACGTGGCATC CTGCCTGTGG TCTGGGTGAG 60
 ATTTACTGTG ACCAGATGTA GAATAAATGT GTCTCATCCT GCATTTTTTT TCTAAA 116

SEQ ID NO:7259

SEQUENCE LENGTH:435

SEQUENCE TYPE:nucleic acid

40 TOPOLOGY:linear

CLONE:HUMGS08498

SEQUENCE DESCRIPTION:

45 GATCACTTTT TAGTTAGTTT GAAACCTGCT TTTAGTTTAT ATGTAGTATT TCTACATATT 60
 GTTACTTAAA TTGAACTAAC AATTACTTTT TNAATTTTNC TTCTTCCTTT TAAAAAAGA 120
 GTATATAATC TGACAATGTT AGTACATCTT TTAGAAGGTC ACTATAAAGT TGCTTTCCCT 180
 ATTTATTTGG AAAGGATTAT TTCCTTATNA TTTTAAAAAA TCTTTTAATT NNTGTCTTNT 240
 CAAGTAATTT TATCATTGTA CCAAGCCTAA GGATGAGTGG CAATTTAAAA GNCACAAGGT 300
 GTGCATCTTC TATCTGCAAA TACTCCAAAC AGAANTTATT CCAGTTTGTT GATACTTTGA 360
 50 GTGGCCAGG GAAAATGTGT ATGGTTTTAG TGTNCTGAAT TGNCATTCCA AAGGGTGCGG 420

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AAGGTTNCTG TTAAA

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SEQ ID NO:7260

SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08499

SEQUENCE DESCRIPTION:

GATCAAAAAA GGAATGGATA TACAAAGTGT TTTGTGAAAT AAAAGCTCCC TAAAATGGTA 60
AA 62

SEQ ID NO:7261

SEQUENCE LENGTH:389

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08500

SEQUENCE DESCRIPTION:

GATCGCACCA CTGCACTCCA GCCTGGGCGA CAGAACGAGA CCCTGTCTCC AAAGGAAAAA 60
CAAAAAAGAA GAATAAAATA ATTTGGATGA AAATCATGTT TATTAAATA GTAATGTCAT 120
GAGACTATTA AAGATGTGCC AGAGTTTCAA TGAAAATCAT TAAAGTAGGA CAGCTAAGAA 180
ATTAATATTA ATATCAAANT TATTGATANT CTAAATTAT TGATTATTCC TTAACGCACT 240
CCATTCTCCT TTACATTTT ATCATGTTTC TTTTGAATAT ATGANTTGGC AAAGGCCTTG 300
ATGAAACTGA GTACTAAGAT TTGGTCCAGN GTATGTCAGG ANGNCACCTC AGATTGCCAT 360
TTTAAATAAN GTTGTNCATG ACCAATAAA 389

SEQ ID NO:7262

SEQUENCE LENGTH:302

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08501

SEQUENCE DESCRIPTION:

GATCCCGTGC TACATCTCCT CCCCGGACGA GTGCCTCTGG ATGGACTGGG TCACAGAGAA 60
GAACATCAAC GGGCACCAGG CCAAGTTCTT CGCCTGNATC AAGAGAAGTG ACGGCTCCTG 120
TGCGTGGTAC CGCGGCGCGN CGCCNCCCAA GCAGGAGTTT CTCGACATCG AGGACCCATA 180
AGCAGGCCTC CAACGCCCTT GTGGCCAACT GCAAAAAAAG CCTCCAAGGG TTTCGACTGG 240
TCCAGCTCTG ACATCCCTTC CTGGAACAG CATGAATAAA AACTCATCC CATGGGTCCA 300
AA 302

SEQ ID NO:7263

SEQUENCE LENGTH:297

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08502

SEQUENCE DESCRIPTION:

GATCGGAAGG TGGTGAATCT TTCCAGAGCA GCTGAAAATN TCAGCATGGA GACAGTAAGA 60

EP 0 679 716 A1

5 AAAGAGACGG GGTGTGGATA AGACTCTGCC ACCGTGTCAC ACTAGCATAG GAGGCTGCAC 120
 GTTCATTGTG TGTTGTTTTT TTTTCCTTTG CCAACCTCCG TTCTATTTAT GTGCAAGCAG 180
 TTTGGATTCA AGTTCTTGT TCTGCTGTT CTGGGACCTG GGGATTGTNA GGGTTCCCTC 240
 ACAGCCAGCA CGACCCCCAG AAAGAGGCGT CCCACAATAA ACACGTCACC TGCTAAA 297

10 SEQ ID NO:7264
 SEQUENCE LENGTH:116
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08503
 SEQUENCE DESCRIPTION:
 15 GATCAACAGT TCTATTACAG ATTAGAATGT TTCACTTCAC AGTTCTTTGT AAATCATGTC 60
 AATTTTATN ATAGNTGTCA ATTTGGGAAA ATCTGTATTA AAATTTTAA ATGAAA 116

20 SEQ ID NO:7265
 SEQUENCE LENGTH:442
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08504
 SEQUENCE DESCRIPTION:
 25 GATCCCTAAT TGGCCAGGCC TGACCCTCTT GGACCTTTCT TCTTTGCCGA CAACCACTGC 60
 CCAGCAGCCT CTGGGACCTC GGGGTCCCAG GGAACCCAGT CCAGCCTCCT GGCTGTTGAC 120
 TTCCCATTCG TCTTGGAGCC ACCAATCAAA GAGATTCAAA GAGATTCCTG CAGGCCAGAG 180
 GCGGAACACA CCTTTATGGC TGGGGCTCTC CGTGGTGTTT TGGACCCAGC CCCTGGAGAC 240
 ANCATTCACT TTTACTGCTT TGTAAGTACT CGTGCTCTCC AACCTGTCTT CCTGAAAAAC 300
 CAAGGCCCCNC TTCCCCCACC TCTTCCATGG GGTGAGACTT GAGCAGAACA GGGGCTTCNC 360
 30 AAGTTGCCAG AAAGACTGTC TGGGTGAGAA GCATGGCAGA GTTTTCCCA GGACAGGTGT 420
 TGACCAGGGC TTNTTGTTA TN 442

35 SEQ ID NO:7266
 SEQUENCE LENGTH:148
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08505
 SEQUENCE DESCRIPTION:
 40 GATCTTCTGA CATTACTGCT GTCTGAGATT TGTATATGTG TAAATACAAG TTCCTTGATA 60
 CCCTAAACC TTGGATTAAG CAGAATGTGC ATTGTACATC TTTAAACAAA ATGTATATTA 120
 ATTTATTAAA TCTAGTTGTC ACTTTAAA 148

45 SEQ ID NO:7267
 SEQUENCE LENGTH:169
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08506
 SEQUENCE DESCRIPTION:
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EP 0 679 716 A1

GATCTTAATT CTGTGTCTTA ACAGCAGGAG ATGAAATTCC CACATGGGAG ATGGCCTCCC 60
 TGTCACAGGA AGGAATANCA TTCTCCCTAT CAATNNGAG AAATTGGAAC TNGAGAATT 120
 CTGTATAGAC CCTTGTCAA GTAATTNTTC TAGTTTAAAN CNTCCCAAN 169

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SEQ ID NO:7268
 SEQUENCE LENGTH:89
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

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CLONE:HUMGS08507
 SEQUENCE DESCRIPTION:
 GATCAAAGAG TCTCATCAA GCAAGTTCTT CCTCCCTGG TCCCCTTGG CTTTCTGAAA 60
 TNATTAATTA AAAGAAAGGC CTTAGGAAA 89

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SEQ ID NO:7269
 SEQUENCE LENGTH:225
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear

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CLONE:HUMGS08508
 SEQUENCE DESCRIPTION:
 GATCATTGNT TTATTTTGT GTCCACCTTT CAATCACTTC ATGTATATAA AAAGGGACTT 60
 TGAATGTAAT AGTCTTCATC TTATTTATTG AAAAGATGTA CTAAGGAAT GACTATTTTT 120
 AAAAAAANT CTAGTATTTA TCAATATGAC TCTAAGGGAA AAATCAAGAA ANTTAGAGGA 180
 AGGTCAANT TAGTAGTAAG GAATAGGANC NNNCATATNA NCTNN 225

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SEQ ID NO:7270
 SEQUENCE LENGTH:259
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08509

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SEQUENCE DESCRIPTION:
 GATCTGTAGT GATGGAGTTC CTTCTGGTGT CAGCCCCACA GGAGGCTCCC AGGCCTCCCT 60
 CACTTCCCAT ACCCAGTCTA GGAGCTCCTT CTGGCTCCA AGCACCAGA GCTTTCCTCC 120
 GCCTTTNAGT TTTGGTTCCT CCACTGGAAT GTAGGCTCCT CACGGGCGAT GGCTGTCTTT 180
 TCTTGACTTT GTATCTTAC TGCCAAGCAA AAAGTCTGCC AAGTGGGAAT NTTAATAAA 240
 TATTCATTGA ATAATGAAA 259

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SEQ ID NO:7271
 SEQUENCE LENGTH:357
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08510

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SEQUENCE DESCRIPTION:
 GATCCCAGAA GGAATGCTGA CCCCTCGTCG TATGACCTGT GCATAGTCTC CAGAGCTTCA 60
 AAGGCAACAC AAGCTCGCAA CTCTAAGATT TTNTNAAACC AAAAAACCC TGGTTAGCCA 120
 TCTCATGCTC AGCCTTATCA CTTCCCTCCC TTTAGAAACT CTCTCCCTGC TGTATATNAA 180

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EP 0 679 716 A1

AGGGAGCAGG TGGAGAGTCA TTTNCCTTCG TCCTGCATGT CTCTAACATT AATAGAAGGC 240
ATGGCTCCTG CTGCAACCGC TGTGAATGCT GCTGAGAACC TCCCTCTATG GGGATGGCTA 300
TTTNATTTTT GAGANGGAAA AAAAAAGTCA TGTATATATN CACATAANGG CATANAN 357

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SEQ ID NO:7272

SEQUENCE LENGTH:265

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS08511

SEQUENCE DESCRIPTION:

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GATCTAAATN AACAGCATTT TTTTCCTTAG CCTCTGTTTG CCACTCTGGG TATCTCTCCT 60
ATGGGCAAAG CCATTAGAAA TGCATAAAAC CTCGAGACAT GGTTTTTGGC AAAAAGTCCA 120
TGACTTTAAA CTAGCTCTTT NACTACTGAC CTTTCACAGA GAAAAAATAT TTCCCTTGAA 180
AAAAAGTGGG CTTGTNATTT TTNCCTTGT AGCTTTAAGC AGAGACATAA GTGCCTTGCA 240
TTACACATAG TAAACTTTCT TTAAG 265

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SEQ ID NO:7273

SEQUENCE LENGTH:164

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08512

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SEQUENCE DESCRIPTION:

GATCTTCTCT TTTTTTGGGT TCATTTTGTT CTGGGTTTTG GTTTTCTTCA CAATCTTGAA 60
CATTTTACAG TAGAACTCAT CTAATAATGG ATTTGGGGAT GGGGAAACAT GCACAAAATC 120
TTTTCATAAT TAAAAAGAGC CTTACTTTCT TTACATACCA CAAA 164

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SEQ ID NO:7274

SEQUENCE LENGTH:243

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS08513

SEQUENCE DESCRIPTION:

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GATCCGTTCC GTGGTCGCC TGCACAACCT CATCAACAAC AAGATTGCCA ACCGGGATGC 60
AGAGANGAAA GAAGGGCAGG AGAAAGAAGA GAGCAAAAAG GATAGGAAAG AGGACAAGGA 120
GAAAGATAAA GATAAGGAAA AGAGTGATGT AAAGAAAGAG GAGAAAAAGG AGAAANAGTA 180
AAACATGTAT TAANTAGCTT TTTTAATTTG TAANTTAANA TCTTACANAC TNGAANCNAN 240
NNN 243

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SEQ ID NO:7275

SEQUENCE LENGTH:265

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08514

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SEQUENCE DESCRIPTION:

GATCACAGGC CTTGAGAGAG NAGAATAAGA CACTCTTGGG GACAGAAAGT TAAAAACCCG 60

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EP 0 679 716 A1

5 TGTGTCCTCA CTTATATGTG GGCCTAAAA AAGTTGATGT CATAGAAGTA TAAAGTAGAA 120
CAGAGGATAT GGAAGGTGG GAAGGGTAGG GGAAGGGAA GGATAGGGAG AGGTTTGTTA 180
AAGGATACAA AATTACCACT CGATAGGAGG AGTAAGTNCT AAGTNCTAGT ATTCTATACC 240
ACTGTAGGAT GACTATAGTT AACAN 265

10 SEQ ID NO:7276
SEQUENCE LENGTH:261
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08515
SEQUENCE DESCRIPTION:
15 GATCGCCCGC ATTCCGGAGC CTTCAAGTAA ACGGCGCGCC CCACGAGACC CCGGCTTCCT 60
TTCCAAGCC TTCGGGCGTC TGTGTGCGCT CTGTGGATGC CAGGGCCGAC CAGAGGAGCC 120
TTTTTAAAGN ACATGTTTT ATACAAAATA AGAACAAGGA TTTTAATTT NTAAAGTATT 180
TATTTATGTA CTTTNATTTT ACACAGAAAC ACTGCCTTTT NATTTATATG TACTGTTTTA 240
TCTGGCCCCA GGTAAGAACT N 261

20 SEQ ID NO:7277
SEQUENCE LENGTH:260
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
25 CLONE:HUMGS08516
SEQUENCE DESCRIPTION:
GATCCACATC TAGTGAAATG TCAGTGTCAA AATATTATAG ATTATAGCTA AAATCCAGAT 60
TAATACTCAT TTGGGGTTTT TAATAGTGA ACTTCATAGT AATACAAAA GCAGATTGTC 120
TTCCTGTCTC CGCTGCTCCC ACAGTAGGTA TTGAACTGG TAAANCAGT TTTTGTATAG 180
30 TGTGTGTATA TAAGANANN TAGATACACA CATTCTTTT CCTCAGTCAN CACATTGATT 240
GACCACTCTG GCAAAGATGN 260

35 SEQ ID NO:7278
SEQUENCE LENGTH:60
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08517
SEQUENCE DESCRIPTION:
40 GATCCCACTC CACCCACCT CAACTTATTT AACTTCCTAA TTAAATCAGA CTGTTTGAAA 60

45 SEQ ID NO:7279
SEQUENCE LENGTH:156
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08518
SEQUENCE DESCRIPTION:
50 GATCTGGAGA CTAAAAAGA AAACAAAAC AAATGGCAAG TTCACTTAA GGGTGGTTTG 60
CCCTTAAGAA GAAAGCTGTT GGGACAAAGA CACCGAGCCA TTATACCAG AATAAAATAA 120

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TACATTTATG CTGGATTTTA TTCAGACCAA ACTAAA

156

SEQ ID NO:7280

SEQUENCE LENGTH:329

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08519

SEQUENCE DESCRIPTION:

GATCATTGTT TAGAATATTT CCGCCACCTT AGAAAGTTTT GTCATGCCTT TTTTTCAGT 60
 CAGTCCCTCC CCTTCACTCA CTGCAAGACC ACCACTGTTG TGACTTTTAG CATCTAAATG 120
 TAGCTTTGGA ATCATGTAGT ATGTACTCTC ATGTCTCTGA AATTCATCCA TGTGTTGCA 180
 TAATTCAGTA GTTCACTACT TTTTAATTC TGATTAGTAT TTCATTGTAT GGGTGTACTG 240
 TAATTTGTTT AACCATTCAC CTGCTGTTTA ATCTTTTGAG CTGTATGCAT TTGGCTATTA 300
 TGAATAAAGC TGCTTTGAAC ATTCCTAAA 329

SEQ ID NO:7281

SEQUENCE LENGTH:270

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08520

SEQUENCE DESCRIPTION:

GATCAGAGAA GACCCCTGAG ATGAATCAGG GCCCTGCCCT GNCCACCAAC TCTTTTCTAG 60
 CAATCATGTC CTGCCCAGGC TGCAGGCTTC ATTAGGCTCC TGCTGTCTC CATGATGTGA 120
 CTAGCACAAG GTGTATATAT GTTTGTACC TCTGCCGATG GCTGTACATA GTGTATGAAA 180
 GTTATTTAAG CCCCATGTTG TACATTCTG TTCCTAGATT GGATGTGTGT GTTCTAAGAA 240
 GTTGTCTATA ATAAACCTG AATGACCAAA 270

SEQ ID NO:7282

SEQUENCE LENGTH:195

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08521

SEQUENCE DESCRIPTION:

GATCCAATTA TTAGAAAAGC ACTCTTAAGA GTGCAATGAA TGTGATTGA AAACCTGAAA 60
 GCAGCCTAGA TTTTACTATA TTTGTTATTG TTATCAATGG GGGTTTGCA ACCTTAAAAA 120
 TTATTTTNA TGTAAGATA CCTAGGAATT TCTAATAACT GTATTTGTTT TAATAAACTT 180
 TGACTTTGCT GTAAA 195

SEQ ID NO:7283

SEQUENCE LENGTH:386

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08522

SEQUENCE DESCRIPTION:

GATCTACCTC AGTTAAACAG TTGGGTGCTA TTAATAAGTC TGTCAAATTA AATTGGAAAA 60

EP 0 679 716 A1

5 AGTAACCAAA CGGTGAGATA CAACTCCACA TGAAACTTGA AATTGTAATT TCGGTTTATT 120
 TAATGATATT TTNATTTATT TGTGCCTTTT ATGTTGAACC CCAATGCATT GAAAAANTTC 180
 AGTATGAAAC AGTACATATT TNATTTATAT TACAGGTGGG AGAAAAGTCC AATTGGTCAT 240
 GGAATTTGAT AGACTTTTCC CCAGCCAAC TGTACAGTGT ATTATAATCC CGACTGCCCC 300
 CCTGTGAAAA GANAAAAAAA ATTGTCCANG GGCAATTTN CCATTNCNA ACCANTANNG 360
 NCCANNCTCC TTTAAAANGN GNGNNN 386

10 SEQ ID NO:7284
 SEQUENCE LENGTH:187
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08523
 15 SEQUENCE DESCRIPTION:
 GATCAGTTAG TAGGCTTTTCG NTGCTTTCTC TTTCAATACA TGTACATCTT TACTGTTTGA 60
 AAAGTGTTAC AGCTGTCAAA GAATCTTCAT GGACCTGAAG ATAATTTNT GTGAAGTTGA 120
 ATGCAAGTNT ACTGTCATTC ATAGTGTTAA TATCAAANTA CCAGGAATNT TNACTTTTNC 180
 20 NACCTNN 187

25 SEQ ID NO:7285
 SEQUENCE LENGTH:113
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08524
 SEQUENCE DESCRIPTION:
 GATCTCAGAA ATTGTATCTN AGTTGGTATC AACCAAATGG AGTGACTTAG TGTACATGAA 60
 30 AGCGTAAAGA GGATGNTTGG CATTNNACT TTTGGCTTGT AAAGTACNGG CTN 113

35 SEQ ID NO:7286
 SEQUENCE LENGTH:120
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08525
 SEQUENCE DESCRIPTION:
 GATCAAAGAG TAAGCCACAC ACGGATAATC AGTTACTAGG GATGGAGGTG TGAGGGTTCA 60
 40 TTATATTATT CATTTTACTG TTGTATATGT TTGAAAATNT CTATAATAAA AAGCTTTAAA 120

45 SEQ ID NO:7287
 SEQUENCE LENGTH:65
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08526
 SEQUENCE DESCRIPTION:
 GATCATGTGT ATGAATTGTT GGTGCTCTAA AGAACAGCAC AAATAAAATN ATTTTCAAAT 60
 50 TTAAT 65

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SEQ ID NO:7288

SEQUENCE LENGTH:110

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08527

SEQUENCE DESCRIPTION:

GATCCGNCCT CCTCAGCCTC CCAAAGTGCT GGGATTACAG GCATGANCCA CTGCACCCGG 60
 CCCCATTCTT CACTTTAGCC TCAGGCAGAG AAGACNGCGC GATGGGGNNN 110

SEQ ID NO:7289

SEQUENCE LENGTH:296

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08528

SEQUENCE DESCRIPTION:

GATCTGCGAC ACTGTGGACT GAACACACTG AAGCTCTGAT GGGAAAACCT GGTGACTGAT 60
 ATAGTTGTTT AGCAATAATT CATAGTCTGT GATGAAGAGT AGTGAATACA ACACACAACC 120
 AGGCAGCCTT CTTGACTATA CTTTGCACAT GNTTCTTTA GGAATTCAC CACACATTTA 180
 AACCAGTTAG TGCTTCTAG AAGAATGGCT TTCCTTTN CTACACAAAN TTTGAATTAT 240
 ACAAGNNTCT AAATATAATA CCTTTNAATA AAAAGGNTAA TTNNGNCCCT CTGAAA 296

SEQ ID NO:7290

SEQUENCE LENGTH:381

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08529

SEQUENCE DESCRIPTION:

GATCAGGTCC AAGCAAAACG TCCAGAGTGC TACAAAATGT TCGTTCTCA GTCCAAAAAG 60
 AAGTGAAAAA GAATCTGAAG TCATGCTTGG ACAATGTTAA TGTGTGTCC GTAGACACTG 120
 CCAGAACACT ATTCAACCAA GTGATGGAAA AGGAGTTTGA AGACGGCATC ATTAAGTGGG 180
 GAAGAATTGT AACCATATTT GCATTGANG GTATTCTCAT CAAGAACTT CTACGACAGC 240
 AAATTGCCCC GGATGTGGAT ACCTATANGG NGATTTCATA TTTNTTGGC GAGTTCATAA 300
 TGAATAACAC AGGAGGATGG GNTAAGGCAA AACGGAGGCT GGGTATGTGT GATGGGAAAA 360
 CTTTCTTCAT TGGTNCCTTC N 381

SEQ ID NO:7291

SEQUENCE LENGTH:51

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08530

SEQUENCE DESCRIPTION:

GATCACCCCC GCCGACGGCC CCGGGCCCCG ACGGCCCGGA AGTCCGCAA A 51

SEQ ID NO:7292

SEQUENCE LENGTH:347

EP 0 679 716 A1

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08531

SEQUENCE DESCRIPTION:

GATCATTCTG TTCTTCAAG GAGAAATAAG CCTAAAAGAA GAAAAACAAA AAAAATTCTG 60
TATAAACTG TAATCCTTG TATTCATGTT TACAGTGCTA TTACTATAAT NCAAAATTAT 120
GTATGTGACT TAGAGTTATA TAATCATAAT TTATGTTTAT TTCAAATATC TAAGTTTATT 180
GCTTGGATT CTAGTGAGAG CTGTTGAATT TGGTGATGTC AAATGTTTCT AGGGTTTTTT 240
TAGTTTGTGTT TTATTGAAAA NTTTAATNAT TTATGCTATA GGTGATATTC TCTTTGAATA 300
AACCNATAAT AGAAAATAGC AGNCACCATA ANCATCTTTG TAAATNN 347

SEQ ID NO:7293

SEQUENCE LENGTH:122

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08532

SEQUENCE DESCRIPTION:

GATCCAGAAA CTTTCCCAA GAAGCTTGA CATGGATTGC TGGTAAACAC AAAAAGTGA 60
TGGAGGGCAG AGCAGCCGGT TGACTCCCC TTGTCAATAT CTTAAAGTGG AAAAGCTTGA 120
AA 122

SEQ ID NO:7294

SEQUENCE LENGTH:138

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08533

SEQUENCE DESCRIPTION:

GATCATCTTT CCTGTTCCAG AGAAGTGGGC TGGATGTCTC CATCTCTGTC TCAACTTTAC 60
GTGTACTGAG CTGCAACTTC TTAAGTTCCC TAACTNAAAG ANCGACTCTG ACAGAAACTN 120
TNTTNCNCA ACAGTTTN 138

SEQ ID NO:7295

SEQUENCE LENGTH:211

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08534

SEQUENCE DESCRIPTION:

GATCCTCCG GNGGAGTGTC GGAGAAGAGA GCTTGCCGAC GATGCCTTCC TGTGCAGAGC 60
TTGGGCATNT CCTTACGCC AGGGTGAGGA AGACACCAGG ACAATGACAG CATCGGGTGT 120
TGTTCTCATC ACAGCGCCTC AGTTAGAGGA TGTTCTCTT GGTGACCTCA TGTAAATTAGC 180
TCATTCAATA AAGCACTTTC TTTATTTTAA A 211

SEQ ID NO:7296

SEQUENCE LENGTH:152

SEQUENCE TYPE:nucleic acid

EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS08535

SEQUENCE DESCRIPTION:

5 GATCAACGGT ACTTGTTTAA AAGAAGCTTA TGTGGACTTT GTCCTTTCTC GTTGCCACAA 60
CCTCTTTTAA TGTGCCTATA GTCCACTATA GCATGCATAT CTCAAATTGC AATTCCTTGC 120
AATTCTGGAA TAAACGCTTT ATTTTGGAGA AA 152

SEQ ID NO:7297

10 SEQUENCE LENGTH:381

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08536

15 SEQUENCE DESCRIPTION:

GATCTGCTGA CTTATATAAA GCTTTTGTAT TCCTACTAAG CTTTAAGATT TAAAAATGT 60
TCAATGTTGA AATTCTGTG GGGCTCTATT TTTNCTTTGG CTTTCTGGTG AGAGAGTGAG 120
GAAGCATTCT TTCCTTCACT AAGTTTGTNT TTCTGTCTT CTGGATAGAT TGATTTTAAG 180
AGACTAAGGG AATTACAAA CTAAAGATTT TAGTCATCTG GTGAAAAGG AGACTTTAAG 240
20 ATTGTTTAGG GCTGGGCGGG GTGACTCACA TCTGTAATCC CAGCACTTTG GGAGGCCAAG 300
GCAGGCAGAC CACTTGANGG AGTTCGGGNC CAGCGTGGCC ACCGTGGTGA ANCCCTGTNT 360
CTNCTAAAAA TNCAAAATTT N 381

25 SEQ ID NO:7298

SEQUENCE LENGTH:379

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08537

30 SEQUENCE DESCRIPTION:

GATCAACAGC CTCCTCTCTT GGGGACTCTC AAGAGCCTGT TTTCATCTAG AAGTAGTAGT 60
TTGATTCTGG TTTCCCTCCT ACAGTGTGTC CTCCGTCTCT TTGCAGCTCC GTCATTACCA 120
TAGGGGACTT GGTTTTAGAC TCTGATGAGG AAGAAAATGG CCAGGGGGAA GGAAAGGTGA 180
35 GTGGGAAGGA GCAGAAAGCT GGGAAAGGGG ATGGGTAGAA CAAGACTGAG AAATCCACAT 240
GCTTCAGANT TCAGAGGGTT CAGGGAATNG TTTGGGATAG TAGGCTCTCC CTGCTCCCTT 300
CTCTACAGGA ATCTNTGGAA AACTATCAGA AGACAAAGTT TGACACCTTG ATACCCACTC 360
TNTGTGAATA CCTACCCN 379

40 SEQ ID NO:7299

SEQUENCE LENGTH:82

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08538

45 SEQUENCE DESCRIPTION:

GATCATTACA AACAAAACT GTAATTTTNT TATATTTGAT TCAATGGAAT TTACCTAAAA 60
AATAAAGACT AAAAATGTGA AA 82

50 SEQ ID NO:7300

55

EP 0 679 716 A1

SEQUENCE LENGTH:225
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 5 CLONE:HUMGS08539
 SEQUENCE DESCRIPTION:
 GATCCCTTTA TTGACAGCCA GTTTGAGGAC ACTGTCCCAG CATCTCTAAT GGAGCCTGAG 60
 CCGGTGTGAG GACCAGGATG TCTTTTCCCA GCCCCAAGAG ACCTGTTGCT GCITTCTTGT 120
 10 AATNATGGGG CTCCCCAGAG TCTGCGTAAC AGTCTCCAC TGGCTGGCTC ACCCAGAGT 180
 GCCATGTGCA CACTCCTGGT TTTCAAACAA TTCTCTGGAT TTAAA 225

SEQ ID NO:7301
 SEQUENCE LENGTH:216
 15 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08540
 SEQUENCE DESCRIPTION:
 GATCATGCAT GCCAATCCCT GTTGCCGCAT GGAGCTCCTC AGCCCACTGA CCTCTCCGTG 60
 20 CCTGGTGCGAG GCCAGGCCCG CGTCTCCGC CTGCCTCTGC TTCCCGTCA TGCATGGTGG 120
 TGGTGTCTTCT ACGGTGTCTG GTTCTGTGCC CGTCTCTGAG ACAGTCTCTG TGTGGAATNT 180
 GCCTTAAACT GAAGTAAATN TGGTTCTTTT AGTAAA 216

25 SEQ ID NO:7302
 SEQUENCE LENGTH:374
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 30 CLONE:HUMGS08541
 SEQUENCE DESCRIPTION:
 GATCAATTCA TGCAAGATAT AATCATATTT TTAAATTAAG AAAATTTTTT TTGTAGAGAT 60
 GGGGTATATG TGTGTTGCCT GGCTGGTCTC AACTCTGGG TCTCAAAGCG GTCCTCCTGC 120
 TTTGGCCTCC TAAGGTGCTG GGATTATAGG CATGAGCCAC TGTGCCAGGC CTGAGGATAT 180
 35 TATCATTATA AATATATATG TACCCACAC TGGATGACCC AGATATAAG CAAATATTAT 240
 TAGATTTAAA GGGAGAAATA GACTCTAATA CAATAGTAGT TGAGGACTTC ACTCTACTCT 300
 CAGCATTGGA CAGATTTTCT AGACATAAAA CCAATAAATA TTGGATTAA ATTGCACTTT 360
 ACACCAAATG GTCN 374

40 SEQ ID NO:7303
 SEQUENCE LENGTH:113
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 45 CLONE:HUMGS08542
 SEQUENCE DESCRIPTION:
 GATCCCATTT CTATGAAATG TCCAGGGCAG GCCCAGCCAC AGAGACAGGG AGTAACGTGG 60
 TGGTTTATTA TAAATTTTTC ATGAAAATAA AATATACAGT ACTCTCGTGN AAA 113

50 SEQ ID NO:7304

55

EP 0 679 716 A1

SEQUENCE LENGTH:286

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

5 CLONE:HUMGS08543

SEQUENCE DESCRIPTION:

10 GATCTGCACA GCCTCTAGAG GCCTCCAGC AAATGCGGGG AGCCATGCCC CCAGGGTCTA 60
CACACTCTCG TTCATCAACA TCACAACTGG AATTCGGGAT TTGTGAAGTT TAGAGCTGNA 120
CAGACTGTGA CAGATTATGA GTCAACACGT ATATTTTCTC TTTCAAAATA ATAATATTTT 180
GTTTTTGACT TTTTACTAAG TGAATATTAT TTTTAAATC TGCCTATATA TTGGAACCTC 240
TATTTTATAA TAATAATGAT AATAAATCAG TACCCAGAAG TATAAA 286

SEQ ID NO:7305

15 SEQUENCE LENGTH:116

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08544

SEQUENCE DESCRIPTION:

20 GATCTAAATN ATGTACTTGT TAGTGATTTC ATTCATATTG ATTGTAAAGG ATTATTTTTC 60
ACTCAGTACT GATGTCCTTG GAAATCTTAC CTGGAAACAT GTTTGCAAAA AACAAA 116

SEQ ID NO:7306

25 SEQUENCE LENGTH:137

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08545

SEQUENCE DESCRIPTION:

30 GATCCCAAGT CTACCCTGGA AATNCCCAGG CACAGCATGC CTGGAGGTGT GAGCCGCCTC 60
TTAGAAGCTT TATAATCCCG GATAATNCTG CTGTAATTGG CATTGTTTTT CCATTACAAT 120
CCTTTCATTA CCTGAAA 137

SEQ ID NO:7307

35 SEQUENCE LENGTH:317

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08546

SEQUENCE DESCRIPTION:

40 GATCCCAGCT TGGTGGGAAA GTGCAGAAGA ATTGCAAAAC TGACATCCCA TNTNACAGCA 60
ATAGTGACCT TTATTTAAAT TGTTGTGTTA TAGTTTATGC TTCTTAAATC ATTTTCAAC 120
NTAAACAGCC AATTTCTAAG CAGACAGGAA AACTAAATAA TAAGTTNATT NATATAACAA 180
AGATGCAGGT TCCTGCTCAT TCCAGTAATG TCTTTGAAAG CANNNCTNAT ATTTNTTTTC 240
TAGATTATCC CTGTGAATAA TTGAGANCTT TTTGGAGTCA AGNATGAATA AAGGTGTGGC 300
AAGGNTATAA ACANNAN 317

SEQ ID NO:7308

50 SEQUENCE LENGTH:337

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08547

5 SEQUENCE DESCRIPTION:

GATCTGTCAG AAAAGACATA TTTTGGAGAT AAAGGAGTTT CTAAATAATG AATTATTGTT 60
 TAGTACCAGC TTTTGGAAATC CTTACATTTT AAGGAACTTG AATAATTTAA ATATTAGATA 120
 ATGTAACCTC TCATAAAAC AGTGTCTAGA CAAGGGCCAA TATTGCATTG AGATTGGATG 180
 AACATTTTAT TTGTCATATA ATTGTTGTCT ATAAAACAAA ATACTAATAA TAATGGCTAC 240
 10 CNGTTAGNCA NTTTAGNNCN TGTCTTACTA TTTACCNNTG TGGNAAAACA TTGCATGNTT 300
 TAATNTTTTT CTAATAAAAT ATTNTNCCAT TANCNNN 337

SEQ ID NO:7309

15 SEQUENCE LENGTH:389

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08548

20 SEQUENCE DESCRIPTION:

GATCCCACCA ATCCTCGTTC CCCCTAAACA TGCTAACAAA AATCCCTTAT TGTGGGTATT 60
 AAAATAATAA CAGTTACACT GTATGCATAT TTATGTGCTC CTTTGTCTG GTTTNCTTT 120
 TCATCATGTA TAAGCTGAAT TCAGCATTAG TTTCTCACAT CTTCCCCCAG GTATCCCCAA 180
 CAGAATTTTT ATGTCCAGC TTGTATTAAA TAGAAGTGAA ATATTAAGGA AAATAAGGAA 240
 25 CTTGTGCAAC TTTTNTATG CATTGTTCTC AACCATTAA TTTATTGAAA GGAGATGCTG 300
 CAACAGTTCT TGATTTAGCA GCAGTTATTC TCTGTTTAC ATAGTTATGG TTTTNTGTTG 360
 TTGGTTTTTG CTCTGGTACT GGAACCGN 389

SEQ ID NO:7310

30 SEQUENCE LENGTH:367

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08549

35 SEQUENCE DESCRIPTION:

GATCCAGGTC TTCTGATTCT TATTCCAGTG TCCTTTCTAG CATAACCATGT TGCCTCTAAA 60
 GATTGCAGCT CTTATTTC TAGAAAATTG TTCCTGCCCC ATCTACATCT CCACCTCACC 120
 CCATCTTTTC TTAAGCACTA TGTTTGTGTT TTTATCAGTA TTATATTCAT TGTCTTTGGA 180
 ATACATGTTT TTGTTTGTGT TTGGAAAAA AATCTCTTTT ACCAGCTTGC ACTCGGACCA 240
 40 ACTTGAAAA AAAAANGCTT AAATGTTTTN GCTATGTNCA GTTTAAAAAT GTGAAGTTTG 300
 TNGCTTTANC TTTTGTAGG AAAATCTANT ANCACTGGCT TAAGTGCTGA CTTGAAATGC 360
 TATCCAN 367

SEQ ID NO:7311

45 SEQUENCE LENGTH:56

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08550

50 SEQUENCE DESCRIPTION:

55

GATCCAGCGA ACCACTGCAC TCTAGCTGGG GAGACAGAGC AAGACTCCGT CTCAAA 56

SEQ ID NO:7312

SEQUENCE LENGTH:92

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08551

SEQUENCE DESCRIPTION:

GATCTCTTCC CTTAGGAAAT ATCAACATCT TTATGTACAT GTCAGAGTCA TGGTGTGATG 60
ACGTACTTTG AAGCATGGAG TCAGTTTTCA AA 92

SEQ ID NO:7313

SEQUENCE LENGTH:368

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08552

SEQUENCE DESCRIPTION:

GATCCACTTA TGAAGTGAAC ATTCTCCATG AACAGGTGGT TGGATTGGTA TCTGTCATTG 60
TAGGGATAGA TAATAAGCTC TTCTTATTCA TGTGTAAGGG AGGTCCATAG AATTAGGTG 120
GTCTGTCAAC TATTCTACTT ATGAGAGAAT TGGTCTGTAC ATTGACTGAT TCACTTTTTC 180
ATAAAGTGAG CATTATTGA GCATTTTNC ATGTGCCAGA GCCTGTACTG GAGGCCCCCA 240
TTGTGCACAC ATGGAGAGAA CATGAGTCTC TCTTAATTTT TATCTGGTTG CTAAAGAATT 300
ATTTACCAAT AAAATTATAT GATGTGGAAA AAAAAAAAAA AATTGCGGGC TTGNANGNTN 360
GGGGTCAN 368

SEQ ID NO:7314

SEQUENCE LENGTH:297

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08553

SEQUENCE DESCRIPTION:

GATCACACCA CTGTACTCCA GCCTGGATGA CAGAGTGGAG ACTCTGTTTC AAAAAACAG 60
AAAAGAAAAT ATAGTTTGAT TCTTCATTTT TTAAATTG CAAATCTCAG GATAAAGTTT 120
GCTAAGTAAA TTAGTAATGT ACTATAGATA TAACTGTACA AAANTTGTTT AACCTAAAC 180
AATCTGTAAT TGCTTATTGT TTTATTGTAT ACTCTTTGTC TTTTAAAGAC CCCTAATAGC 240
CTTTTGTAAC TTGATGGCTT AAAATTCCTN ATTAATNCTG CCATTTCAN TTCCAAA 297

SEQ ID NO:7315

SEQUENCE LENGTH:86

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08554

SEQUENCE DESCRIPTION:

GATCTTTGAA TGAGCTTTTT AAGGAAGAAA TATTATATAT TGTTTGTTAA AGTTTATTGA 60
AATAAAGAAT CATTAAATC TTCAAA 86

EP 0 679 716 A1

SEQ ID NO:7316

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

5 TOPOLOGY:linear

CLONE:HUMGS08555

SEQUENCE DESCRIPTION:

10 GATCCAAATT GTGAAGCCGT TGGTCAGGTG CCTGGCTACA CACAAAATGG TGGAGGCTTA 60
GCCTAAACAG TTTCTTCATT TCACATTAAA ATCCTAATTN NTGGCTCCTC TCAAAATGAG 120
TTCTAGAAGC ACNGGNTGTA GATTCCCATG TGGACACAGC CTTCAGGAGG TGAGCAGCAG 180
CTCCCTGCAG CCAGCTGGAG CCTGCCAGTT TTCCCTAGTG CCCAGCACTC CTGAGCTTCT 240
GCCCTCCGAG GGATTCCCGA AGTTTTTCT AATGGGNTTA GTGGNGNCNC CTTTGGGGTT 300
GCTTNGGTTT CTTTTNGTTA NGNGCCCTTG NTTTTAAATT AAANCNGGGC CATTNN 356

15

SEQ ID NO:7317

SEQUENCE LENGTH:349

SEQUENCE TYPE:nucleic acid

20 TOPOLOGY:linear

CLONE:HUMGS08556

SEQUENCE DESCRIPTION:

25 GATCTGTGGG ACTGTCTGGG CCTGTTACTC ATCCTGCTAT CAATTTCTTA TTAATTAATC 60
TTGATGATTC TNATTAATTA ATCACATTTG CAGGAAATTC AGATGAGGCA AGAAAATTTN 120
ATTGGCCTGG GNNNGACTGA AAGCATTCCA AATTAGGCTT AGACTGTGCA AAGGGCTTAG 180
CTAAGTTATC GAGCTTAAAA CCCGTCAATT AANCAACAT TATTGANCE GTTACTGCAT 240
GCCACGCACT GTGTTGGGCT TAGTAATAAA ANNNAGNAAA GGTAAGNGCT TGTNCTNGCC 300
TAAATTAAAG GGTCCCCGGG GGTTTTTTCT NGAGGGGGCN NCTGCCCCN 349

30

SEQ ID NO:7318

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

35 TOPOLOGY:linear

CLONE:HUMGS08557

SEQUENCE DESCRIPTION:

40 GATCACCTGA GGTCAGGAGT TCAAGACCAG CCTGGCCAAC ATGGTGAAAC GCTGTCTCTG 60
CTAAAANTAC AAAANTTAGC TGGGCATGGT GGTGGGCACC TGTAATCCCA GCTACTCGGG 120
AGGCTGAGGC AGGAGANTCG CTTGATTCCA GGAGGCAGAG GTTGCACTGA GCCAAGACTG 180
CACTGTTGCA CTCCAACCTG GGCAACAAGA GCAAACTCC GTCTCAAAA AAAANGTGTT 240
TAATTATTCT AAAAAAATT CAGCCAGGTT ATTCCAAATT NTAATTGAAA NCNGGGGGCC 300
CAGGTTAANC GGGGCCTTAC CTTCCCTTN GCNCTTTGGA NTTNNCCAT N 351

45

SEQ ID NO:7319

SEQUENCE LENGTH:333

SEQUENCE TYPE:nucleic acid

50 TOPOLOGY:linear

CLONE:HUMGS08558

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SEQUENCE DESCRIPTION:

GATCAGCAGT GTTGACCATT TATGCTGCAT AGCTGGTATT ATAGCCTTAT TAGTTGTGTG 60
 GTTGACCCTT GGGGTATACA AATGTCAGTC TGAGTGGTGN CTTACTCCTT TGTTTATAAG 120
 TGAATGATTG TGCATGTTTT GTATGTCATA GTATGTCGTC ACATAAAAGG GAGGGAGCGA 180
 AAAACCATTA CATTAAAGATA ATATTGGACC AAACACTTA CTTGCTCTAA ACAGTTACTT 240
 GTACCCCTTA ACCTGTCTTC AAAAGTTGCA TATAGTTACA GTAGTGATA AATTAAATAT 300
 TGTGGAAAAC CANNAANNN NNNNANNNN NNN 333

SEQ ID NO:7320

SEQUENCE LENGTH:192

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08559

SEQUENCE DESCRIPTION:

GATCAGCTGA AGGTTTCATGG GTTTTAAGTG CTTGTGGCTC ACTGAAGCTT AAGTGAGGAT 60
 TTCCTTGCAA TGAGTAGAAT TTCCTTCTC TCCCTTGTC CAGGTNTAAA ACCTCACAGT 120
 TGATAATGTA CCATTGGGGN CCGTTTAAAC TGGGCCTAGG NACCCCTCA NGAATAACCT 180
 GNAAGGGCCA AA 192

SEQ ID NO:7321

SEQUENCE LENGTH:55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08560

SEQUENCE DESCRIPTION:

GATCGTGCCA TTCCACTCCA GCTTGACAA CAAGAGCAA ACTCCGTTA TTAAC 55

SEQ ID NO:7322

SEQUENCE LENGTH:78

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08561

SEQUENCE DESCRIPTION:

GATCAGACCC CCACAATATG TCTCAACCTC TGTGAAGGG CTAGTGATGT TAAAAAAC 60
 CTGTTATTTC CAATCAA 78

SEQ ID NO:7323

SEQUENCE LENGTH:375

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08563

SEQUENCE DESCRIPTION:

GATCTGGTAT TTCCTGGACT AAATCCCCT TGGGAAGAC GAAGGGATAN TGCAGTTCCA 60
 AAAGAGAAGG ACTCTCCAG AGTCATCTAC CTGAGTCCA AAGCTCCCTG TCCTGAAAGC 120
 CACAGACAAT ATGGTCCCA ATAACGACT GCACCTTCTG TGCCTCAGCC GTTCTTGACA 180

5 TCAAGAATCT TCTGTTCCAC ATCCACACAG CCAATACAAT TAGTCAAACC ACTGTTATTA 240
 ACAGATGTAG CAACATGAGA AACGCTTATG TTACAGGTTA CATGAGAGCA ATCATGTAAG 300
 TCTATATGAC TTCAGAAATG TTAATAATAGA CTAACCTCTA ACAACAAATT AAAAGTGATT 360
 GTTTC AAGGT GGAAA 375

10 SEQ ID NO:7324
 SEQUENCE LENGTH:271
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08564
 SEQUENCE DESCRIPTION:
 15 GATCCACCTG CCTCGGCCTC CCAAAGTGCT GCGATTACAG GCATGAGCCA CCGCGCCTGG 60
 CCGCTTTCGA TATTTTCTAA ACTTTAATTC AAAAGCACTT TGTGCTGTGT TCTATATAAA 120
 AAACATAATA AAAATTGAAA TGAAAGAATA ATTGTTATTA TAAAAGTACT AGCTTACTTT 180
 TGTATGGATT CAGAAATATAC TAAATTAAT TTTTAAACA CAACTTTTAA AAAATGTATC 240
 AAAATAATAA ACGTGTCTG ATATTTTAA A 271

20 SEQ ID NO:7325
 SEQUENCE LENGTH:102
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 25 CLONE:HUMGS08565
 SEQUENCE DESCRIPTION:
 GATCCCCTGA GTTCAAGAGT TTGAGACCAG CCTAGGCAAC CTTGTCTCTA CAGAAAAATA 60
 AATAAATAAA TAAATAAACA AACAAACAAA CCAAAAATTA AA 102

30 SEQ ID NO:7326
 SEQUENCE LENGTH:216
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 35 CLONE:HUMGS08566
 SEQUENCE DESCRIPTION:
 GATCATGAGG TCAGGAGACC GAGCACCATC CTGGCTGACA CGGTGAGACC NCGTCTNTAC 60
 TAAAAATACA AAAGCAAAAA TTAAGTGGGT GTGGTGGCGG GTGCCTGCAG TCCCAGCTAC 120
 TNGGGAGGCT GAGGCAGGAG AATGGCATGA ACCTGGGAGG CGGANTTGCA TTGAGCTGAG 180
 40 ATGGCACCAC TGCACTCCAG CCTGAGCGAN NNNNNN 216

45 SEQ ID NO:7327
 SEQUENCE LENGTH:176
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08567
 SEQUENCE DESCRIPTION:
 50 GATCTGCTCT CTGTTGAGAG TTGGTAATCA TTGGTTTGAA ATGTGATGAA ACCACTCAAG 60
 CCAATGAAGG TGGGTGTGTA GGTGGGGAGT ACTTTGCCAT AATATTTTAA AACATTACCT 120

55

GGTTAGAGTT CTAAGTGGA CTTATTTTGG TTTGGTTAGG GGAAAGCCTG AATAAA 176

SEQ ID NO:7328

5 SEQUENCE LENGTH:106

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08568

SEQUENCE DESCRIPTION:

10 GATCTCTGGC TGTTTGATTT TTTTATATTT GTATTTTAA AATNTGTAA ACAGTGCCCT 60
GTGAGCACCA AGTACCACTA GATGAATAAA ACGTATTATA TCTAAA 106

SEQ ID NO:7329

15 SEQUENCE LENGTH:379

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08569

SEQUENCE DESCRIPTION:

20 GATCCGGCAG GCAGAGAGGA AAAAGGGAAC TTGTACCAAG CACAAACAGG NTCTAGGCAT 60
AGTGCTGTGT ACTTAGGTTT TTCCTGTGCT TCAGTCTTTC CAATAAATCC AGGGGTAGG 120
TTTAAATCTN NCTATTTNAT AGTTACAGAC CATTTTAAAT GGACAAGCAG CCCATTTAAA 180
GATAAAAGTA CTTAGATGGA CTAGCAGCTT CTCTACCAA TTATTTACC ACACAAAGNT 240
25 AACATCATTG TGAATTTGG TTTAGTTAAC ATGCATTCCC TGGCCTGCCT CACACCGGAC 300
CTNTACCCGG TACCATGCAA ATGCACATCT GCTGCTACAC TTGTGGGATG CTGGTTTAGG 360
TAATTNTTTT TTATAATNN 379

SEQ ID NO:7330

30 SEQUENCE LENGTH:271

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08570

SEQUENCE DESCRIPTION:

35 GATCCCAGCA GAATACAAA ATCCTATTTT TTTTGACTGA GTATTTGTAG ATGCTTAATG 60
ACTGAAATNA ATTTGGAGGC ACTGATGAAA GTAATTTTTT NAAAGTTCTC AGGTACTGTT 120
CAATTATTTA ATGTTAAGTT TAGTATCAAG ATACAGTTGT TTTNAAAATG CCAAATGCT 180
GTTTATNATA CAGAATATTT NATTACATTT GCAATATCTT TGTATATAGT GATTTTNTNC 240
40 TTGATAATAA ATGGAAAANT TCTAAACCAA A 271

SEQ ID NO:7331

SEQUENCE LENGTH:382

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08571

SEQUENCE DESCRIPTION:

50 GATCGACCTG CCTCTGCTTC CCAAAGTGCT GGGATTACAG GCGTGAACCTA CCGCGCCTGG 60
CCCTCAGATA TTTTAAATTT TGAATAATTA GAGTATATAT TAATATCAAG TNGCAGAAAC 120

55

EP 0 679 716 A1

5 AGAATGAAGT GTTATAAAGG CGTAAAGTAG TAGGGNGGCA TAAAACTTAA ATCTTTAAGC 180
TAGAAATAGC TTGAGGAATT ATCTGATGCA GTACTCTGTT GTAATATAAC AAAAATGGAA 240
TCACAGTTTT ACAAATCAGG CAGCTGCAGC TCAGNGAGGT TAAATTTCCA CAGACCTGTT 300
TATGCAGCGC GGTAANTGAG GAAGTAGACC TAAAATTGG GGCCTCTGCT ACTCTGGGCC 360
ATTACCTCAG CCTCGCTGGC AN 382

10 SEQ ID NO:7332
SEQUENCE LENGTH:315
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08572
SEQUENCE DESCRIPTION:
15 GATCTCACAG GAATCCTTCA ACTGCTTTCT ACCAAGCGTT CCATTTGAAC ACGTTAAAGG 60
AATCAAAGAG CCTCTGGGAT AGGGGGGAAA NCACATGGTA TCTAGCATGG GACAAAGCAG 120
CAAAATAAAC CAAAAGGACA ATCTCTATTT TATATAGAAA ATAAACATAC TTTTCTGCAT 180
CCTGTGTACT TTAAGTATAT CTATATTTTT GAAGGGTTCA TACTGTGTTG AATTTTCTT 240
ATGAAATAGT CACTTCCCCA GTGTATTTTA ATGCAAATGC ATATTCTATA AAATAACCTA 300
20 TATTTTAATT TAAA 315

25 SEQ ID NO:7333
SEQUENCE LENGTH:104
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08573
SEQUENCE DESCRIPTION:
30 GATCTTTAAT ATCTGATATA TTCCTGGTAC TCGTACTGAT AAGGGATTAT TGGAAGTCAG 60
TCACAGAATT TGGAATAAA TTCTAGTCTN TCCTTAGCTN NNNN 104

35 SEQ ID NO:7334
SEQUENCE LENGTH:140
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08574
SEQUENCE DESCRIPTION:
40 GATCTACCTG AGGCTCAGTC CTCATCTGTA AAATGCTGAT AAAAGGACCT ACCACCTAGC 60
GTTGCTGTGA GGTGTCAGTG AAATAAAATG TAAAATGCTT AGCACAGTGA ACTTTAATAA 120
ATGGTAGTTG TGGTTGCAA 140

45 SEQ ID NO:7335
SEQUENCE LENGTH:93
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08575
SEQUENCE DESCRIPTION:
50 GATCTAAAGT CTAATAAACA AATCCTTAGG TTAAGAAGAA AATAATGCAA TAAATAAAAT 60

55

GTTATAAATA AATGACATAT TGCNACTTTT AAA

93

SEQ ID NO:7336

SEQUENCE LENGTH:96

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08576

SEQUENCE DESCRIPTION:

GATCATACCC ATGAAACCCA CTGTTTAGAT TTTAAAAAGT TCAATGTTTT TCTGTATTN 60
ATCTCTTCAT TTTAAATAA AGTTTTGCAC ATGAAA 96

SEQ ID NO:7337

SEQUENCE LENGTH:224

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08577

SEQUENCE DESCRIPTION:

GATCTAAAAG CAGATGCTGT AGCTGCCTAC TTAAACCCAT TTTTCAACCT GTTTGTTTTT 60
TAAAGGGCTT CACTAAGGGT NNNNNATGTA CCATTGTAGG GGGCAATTTT AAGTCAGCTA 120
AGGCAATAAC CTTATGCATG AACATTTCCC AGACTTTCAT GAAGCTGTTG AGGTCCTAGG 180
CAATTAATGC GGCAGTTGTG ATAAATAAAA ACATCTCACC TAAA 224

SEQ ID NO:7338

SEQUENCE LENGTH:175

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08578

SEQUENCE DESCRIPTION:

GATCNATATT TAGTGACTGC AACATGTTTA TACCACTGAT TCAAATTCCA NNNNTGATGA 60
AGTTATACAA ATAATGCATA TATTGATAAC TTTTATTGCA AAAATGTAAA TTTAAAACTT 120
GTATAATGTT CTTGTGCTTT TTTAAATAAA ATATATGTGT ATATTTAAAA AGAAA 175

SEQ ID NO:7339

SEQUENCE LENGTH:143

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08579

SEQUENCE DESCRIPTION:

GATCTGAGGA TGGTTATAAA TACTGTAAAGT ATTGTAATGT TATGAATGCA ANNNTATTTG 60
AAAGCTGTTT ATNATNATAT CATTCTGAT AATGCTATGT GAGTGTTTTT AATAAAATTN 120
ATATTTATTT AATGCACTCT AAA 143

SEQ ID NO:7340

SEQUENCE LENGTH:106

SEQUENCE TYPE:nucleic acid

EP 0 679 716 A1

TOPOLOGY:linear
 CLONE:HUMGS08580
 SEQUENCE DESCRIPTION:
 5 GATCACTTGA TTTTAAAGAA ATNAAAAATT GCACTAGGTA GAAATAGTGT ACCAGGCAAT 60
 AGTCCAGCTT TAGTTTTNTG TCATTTTNG TCTCTATTTA AAGNNN 106

SEQ ID NO:7341
 10 SEQUENCE LENGTH:93
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08581
 SEQUENCE DESCRIPTION:
 15 GATCTCAAAG CAAATCTGTA TTTAATCTC TCAGGTGTTT ACTAGTATTA CCAGTGACTA 60
 GTGGAAATAA TAAAAGGAAA TCTTGTTTCA AAA 93

SEQ ID NO:7342
 20 SEQUENCE LENGTH:193
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08582
 SEQUENCE DESCRIPTION:
 25 GATCTTCGCT CCAGCTTTCT GCATCTGAGC TGGAAAAAGA GCAAAAACGG GTAAAAATTG 60
 AATCCAAATA TTGTCGNATG TATGCCTAAT TTAGAATGAA ATCTTGGGGT GGCAGACTCT 120
 GGAGTTCTCT GTGAGGTGTG GCATTCTTT NTCTAAATCA CTTATTGGCC AATGTATGTG 180
 TCACTTTGTT AAA 193

30 SEQ ID NO:7343
 SEQUENCE LENGTH:137
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 35 CLONE:HUMGS08583
 SEQUENCE DESCRIPTION:
 GATCTATAAT AAGAGCTCAA TAACTNNGTC AAGGAAAGCT CTAATATATG CAGTGATGGT 60
 TTATGAAAGG GTGTGGCAAT NTNAAATNTA TATTGTGTGT GATGTTCAAA TAAAGTGGTA 120
 40 TCTACATNCA TGTGAAA 137

SEQ ID NO:7344
 SEQUENCE LENGTH:389
 SEQUENCE TYPE:nucleic acid
 45 TOPOLOGY:linear
 CLONE:HUMGS08584
 SEQUENCE DESCRIPTION:
 GATCCCTGGT ATNGTCCGAA TTGTAAAGAA CATCAGCAAG CCACAAAGAA ATTGGATTTA 60
 50 TGGTCCCTGC CTCCAGTACT TGTAATACAT CTNAAAGCNAT TTTNTTACAG TCGATACATG 120
 AGAGACAAGT TGGANACCTT AGTTGATTTT CCTATCAATG ACTTGGATAT GTCGGAATTC 180

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TTAATTAATC CAAATGCAGG TCCTTGCCGC TATAATCTGA TTGCTGTTTC CAACCACTAT 240
GGAGGGATGG GAGGAGGACA CTATACTGCT TTTGCAAAAN ATAACGATGA TGGAAANTGG 300
TACTATTTTG ATGACAGTNG TGTCTCCACT GCATCTGANG ACCAAATTGT GTCCAAAGCA 360
GCATNTGTAC TCTTCTACCA GAGACAAGN 389

SEQ ID NO:7345
SEQUENCE LENGTH:367
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08585

SEQUENCE DESCRIPTION:
GATCTGTTAC CATCAGGTCA ATTCCTAGTA TGCATAAAATT TTTTAACCCT TTTAAAAGAG 60
ACCTATGTTG AAAACCCCTG AAAATTCACCT GAAGAAAAAT CATTACTCTT NTTCTCNGTA 120
AATCATATCA TCTGAAATAT TACAAATTTT AAATTTCTAG GTGCTATATT AATTCAATAT 180
TACAATAACT CTTACCTAAT TATCTTACA AGTTTTAAGT TGTGGTAGTT TAGTGATTTT 240
TTTAAAAGAT GTGTGAAATG TTCTCTGCAA AATAATTCAG GCCACTGTCT CCTTTTATAT 300
ATNATNATNN TNGTNTGTGA TGANGACCAG TGAATTACGA TATTTAAAGT GAGAGACCTT 360
AATTNTN 367

SEQ ID NO:7346
SEQUENCE LENGTH:23
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08586
SEQUENCE DESCRIPTION:
GATCCCGTCT ATAATCNAAC AAA 23

SEQ ID NO:7347
SEQUENCE LENGTH:103
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08587
SEQUENCE DESCRIPTION:
GATCGGCTCC CTGTCGCCGCC CGAGGAGGGC TGGACCTTTC GTGTCGNACC CTGGGGNGCG 60
NNGAGACTGG GTGGGGAGGG TGTGAATAA AAGGGAAAAT AAA 103

SEQ ID NO:7348
SEQUENCE LENGTH:367
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08588
SEQUENCE DESCRIPTION:
GATCTGGTGG CTGGAAAAAC AAGAGTGACA TTAACAAATC ACAAAAAATC AGTTAGGGCT 60
GTGGTTTTAC ATCCAAGACA TTACACATTT GCATCTGGTT CTCCAGATAA CATAAAGCAG 120
TGGANATTCC CTGATGGANG TTTCATACAA AATCTTTCCG GTCATAATGC TATTATTAAC 180

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ACATTGACGG TAAATNCTGA TGGAGTGCTT GTATCTGGAG ACAGAAGAAA CTCATCCAGT 240
CAGCTGGAAA CCAGAAATTA TCAAGNGAAA GNGATTTTAA TGAATGTGGA ATTTTTCCTC 300
TCTCTTTTTT TTTCTTTTAA ATTAATAANAA AAAAGGCTTG GNGTTCATGG GGGNTTTCCTC 360
GNCCTTN 367

SEQ ID NO:7349

SEQUENCE LENGTH:22

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08589

SEQUENCE DESCRIPTION:

GATCCCGCCT NTTTCTTACA AA

SEQ ID NO:7350

SEQUENCE LENGTH:378

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08591

SEQUENCE DESCRIPTION:

GATCTTTTAA AAATTCATCC CATATCCAGA AAGTACCAGT TATAAAGATT GCTGACCAAG 60
CAAAGTTTGG CATCAAAGTG TCACCTCATT GCTCTGACCA AAGACTGACT GTTGTGGTTT 120
TAACTCCTCT CTGTAAAGCA TTTTGCATT TCCCCAAGCT CCTTCTGAA AGAAGAACCA 180
GTGCAGAGCG GCCTTTACTT TCAATTTCTA CTGCTGAATA GACTACTTAG AGAAAATGTG 240
AGTTTCAGTG TGAACAGAAT GGATTAGGAT GACGAGTTTG ATGGGCATTT TCAGTACTGT 300
ATCTAAGAAA AAAAAATTNG CACAGCTAGG AGCCTCTGAC CATTGTCTGG GTGTTTACG 360
TGGGTCCTGT TCATCAAA 378

SEQ ID NO:7351

SEQUENCE LENGTH:379

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08592

SEQUENCE DESCRIPTION:

GATCAAAGTC AAAAAATGCA ATGNCTCCCT ATCCCTCACA CATCCAGACA TCATGAATTT 60
TACATGGTAC TCTTGTGAG TTCTATAGAG CCTTCTGATG TCTCTAAAGC ACTACCGNTT 120
CTTTGGAGTT GTCACATCAG ATAAGACATA TCTNTAATC CANCCATAAN TCCAGTTCTA 180
CTATGGCTGA GTTCTGGTCA AAGAAAGAAN GTTTAGAAGC NNNNNCACAA AGGGTTGGGA 240
GCTGATGAAA CTCACAAATG ATGGTAGGAA GAAGCTCTCG ACAATACCCG TTGGCAAGGA 300
GTCTGCCTCC ATGCTGCAGT GTTCGAGTGG ATTGTAGGTG CAAGATGGGA AAGGNTTGTA 360
GGGTGCAAGC TGTCCCAAN 379

SEQ ID NO:7352

SEQUENCE LENGTH:119

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS08593

SEQUENCE DESCRIPTION:

5 GATCTGCTTT AGTGAGAGGA CAATTTCTGA TTGATTGTTT TCTCTTCAGG CCATCTCACC 60
TCTTCATTCT CTTGTNACAT TTGAAGCAGT TGATATAATG GGTTTATANN NNTAAAAGN 119

SEQ ID NO:7353

SEQUENCE LENGTH:93

10 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08594

SEQUENCE DESCRIPTION:

15 GATCAGCTAT TTTCAACATA ACTGAAGGCA TATGCTGGCC CATAAACACC CTGTAGGTTT 60
TTGATATTTA TAATAAAATT GGTGTTTTGT AAA 93

SEQ ID NO:7354

SEQUENCE LENGTH:297

20 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08595

SEQUENCE DESCRIPTION:

25 GATCTCTGTA GACTTGCCCTC TTCTGGACAT GACATAGAGA AAGGAGTCAT AAATTCTCCA 60
AGGTGTCTGT TTCTTCTTTA ATGTCATTCC CTGTTTCTCC TCACATTCCC TCCCCATTTC 120
CTGGGCCCAG TCTCACAAGT GTCCTTGCTT ACCCTAAATG CTATTAATTC CATCACTCTG 180
AGTATGGTGT TTGCTGTCCG CTGAATGCCA AGAGCTTCAA GAGTGTGTGT AAATAAAGCC 240
ACACCTTTAT TTTTGTATTA TTCTGAACCA TGGCTAATAA ATTGTTTCAC CAAGAAA 297

30 SEQ ID NO:7355

SEQUENCE LENGTH:45

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

35 CLONE:HUMGS08596

SEQUENCE DESCRIPTION:

GATCTCCGAT GTGATGAATA CGAATAAAAG GCCCTTAATG GCAAA 45

40 SEQ ID NO:7356

SEQUENCE LENGTH:212

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08597

45 SEQUENCE DESCRIPTION:

50 GATCTGTTCA TGCTTTTGTG TTCGTCACTG CGGCGGGGCC CTTTGATGTC TTCATCTGTA 60
TGGGGTGGAA AAATCACCGG GAATCCCCCT NNNAGTTCTT TGAAAAAGTT CCATGACTCG 120
AATATCTGAA ATNAAGAAAA CAAACCGACT CACAAACCTC CAAGTAGCTC CAAATGCAAT 180
TTTAAATG GAAAAACAAA ATCTGAAAGA AA 212

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SEQ ID NO:7357
SEQUENCE LENGTH:250
SEQUENCE TYPE:nucleic acid
5 TOPOLOGY:linear
CLONE:HUMGS08598
SEQUENCE DESCRIPTION:
GATCTAAACT GTATTTTCCA ATTTAAATTA AAAATGTAAT ATAGATTCAG AAAGGTTTCAT 60
10 ATTTTCTTAA TGAATTCATT CTATATTATT TTGTTAGGTT GCATAAAGAA GCAAGGAATT 120
GTACTTGTAT TAAAAGATGA GGAAAGCTAT TAGGNTTATT GGNCCATGCC TGAATNNGG 180
CCTTTGCCCG TAAAAGGAA AGGTTGGCCC NTTTTNAAG GGGGCNTTNA TNTGNNTTN 240
TNTTAACCAN 250

15 SEQ ID NO:7358
SEQUENCE LENGTH:112
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08599
20 SEQUENCE DESCRIPTION:
GATCTGGCTT NGCCCTAAGC NNCTTAGGNA CAGAAGAGTC CATGGGGGCA TGGCACAGAG 60
CTGGTCCTGT ATTCTCCAGG GTCCGGAGCT GGCCAGGGGC GGGGAGGAGG NN 112

25 SEQ ID NO:7359
SEQUENCE LENGTH:386
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08600
30 SEQUENCE DESCRIPTION:
GATCTTATTT NACTTCATCC TTCTTGTAAC CATATTGTNA ATCAGGAAAG CTCAATCAGA 60
TACAAAAACA GGAAATTCGT TAAAAGTAAC GTTTGTAGAA GATACTAGTT GAGGAGGAGA 120
GACTTTTNG AGGCCTGTG TGTGTTTGT AACTCTTGT GACCGTGCCA AGAAAACGTA 180
35 AGCAAATATC AAGCCTCCAA ATCCTAATGC AACANGTCCT GANTCCCTTG CAGGTATGTC 240
CTGGATGATG ANTACACAAG CTCAGTAGGC TCCAAATTC CAGTCCGGTG GTCCCCACCG 300
GANGTCCTGA TGTATAGCAA GTTCAGCAGC AAATNTGACA TTTGGGCTTT TGGGGTTTTG 360
ATGTGGGAAA TTTACTNCCT GGGGAN 386

40 SEQ ID NO:7360
SEQUENCE LENGTH:341
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
45 CLONE:HUMGS08601
SEQUENCE DESCRIPTION:
GATCCGGGNA TTATACAGGT ACTGTTGGAA GTATCTTGGG GATTTTCCTG ATAAGAACAG 60
TAGTGATTGN ATAAAAGGA CAGGATGTAA AGTGAAATCA GTAAATATC TTAGTAGACA 120
GAGGGTGCTG AAATTTTAAC AAATGTGTAA AAAGTTCTTC CTATGCATTA ATTTCCAGA 180
50 TACCCTTAAA ATGTTTAAGG AATGTAATC AAAATACTGT TTAANAGAGA CATGTGACCA 240

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TCATTCTCCC AGCGAATGTG AATCATTTAG TNGGCTACTC AAAATTAGGN GTAAATGTAT 300
 ATGTACACTA TAAGANTAAN ANTCGNTACC ATTTCTTTAA A 341

5 SEQ ID NO:7361
 SEQUENCE LENGTH:92
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08602
 10 SEQUENCE DESCRIPTION:
 GATCCGTCAG NCGACTCTAA AGCTAATTGT TTGTATTGGC ATGGNTTTTG CCAGGCATCC 60
 AAAATTGAGA TTAACAACC AATGCAATCA AA 92

15 SEQ ID NO:7362
 SEQUENCE LENGTH:359
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08603
 20 SEQUENCE DESCRIPTION:
 GATCTCGTCT GAAACAGTGT TTGGAAGTGG GAACAGTTTT GTCCTGTATG CTGATGTGTC 60
 CAGAATTTCA TTTAATGATA GACGGAAAAT GTGTGGTTAC TGAAAACTGT ATATGATACA 120
 GAATTCATA AGAGCCATGC TGTGGGGCAA AGCAACTCTT TTTCAACCAC TGCTCATCAG 180
 25 TTTCTGTAGA GACAAAACT CTGTACATAT TTTGGAATCT GAAGAATCCT ATGTAAATCA 240
 TTTGTTACTT AAGTCTGTGA AAAACATATT TCTTTGGAGG AAAATGTATG CATTATAAG 300
 TGTTCCATGG AATCAGTTTT TATTGTATCG ATATAATTGT CTCTAAGTGT TGACTGTCTN 359

30 SEQ ID NO:7363
 SEQUENCE LENGTH:273
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08604
 35 SEQUENCE DESCRIPTION:
 GATCTCCTTA CACTGCTATT CCAGAGGAGA AGNCACCAGG TCACTCAACT CTTAGTATCA 60
 TCTACTGGAA ACTGGCTAAG ACAGTATTTA TGTGCTTCTC TCACAATAAC AGGAAGATAN 120
 CTATATCACA CAATGGATAT GGCAGTTGGC TTGACTGCAG TAATCATTTA ACTATGTATA 180
 TGTATATCAA AACATCATGT TGCATACCTT AAATATGTAC AATAAAAAATA AAATCTAAAG 240
 40 GANATAANTT AANATTACCT TCCACCAGGC AAA 273

45 SEQ ID NO:7364
 SEQUENCE LENGTH:358
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08605
 SEQUENCE DESCRIPTION:
 GATCAGGGAT GCAGTACCAC TTGCAGTCAA ATGAATTCCT TCGAAATGTA TTTNNACTTG 60
 50 GACCCCCAGT GATGCTTGAT GCTGCAACGC TTAAAACGAT GAAGATTCTT CGTTTCGAAA 120

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GGCATTATA TAACTCTGCA GCCTTCAAAG CTCGAACCAA AGCTAGAAGC AAATGTCGAG 180
 ATAAGAGAGC AGATGTTGGA GAATTCTTCT AGATTTTCAG AACTTGAAGA CTATTTTCTA 240
 ATTTCTATTT TTTTCTCTAN TTCAATGTAT TTAAACTCTA GACACAGTTT TTATCCTGGA 300
 TTAACCTAGA TAACTTTTGT AGCAGTGGTT ATATTGCTTA TAATTTAATG TACAATTN 358

SEQ ID NO:7365

SEQUENCE LENGTH:263

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08606

SEQUENCE DESCRIPTION:

GATCTACNGT GAATATAAAA TGTATTAGC CTTATCAAAT AAATAAATGA GCANAGCTCT 60
 TTGTTGCTC TATTGAACTG GGTGATAATN ATTTAGATGT GAATGTTAGG TCAGTTCTAC 120
 TGTAATAACT AATCGTAAAA GTTGTAATN TGTTTAATGG ATGAAATGTA CANTTTTTGT 180
 ATTCTNTACA GCTTTGTCTT TTTTAAATAT GAAGTACTTA AATGTACTTA CTATGATAGG 240
 AAATATAATG TGTGCCTTCT AAA 263

SEQ ID NO:7366

SEQUENCE LENGTH:366

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08607

SEQUENCE DESCRIPTION:

GATCTAAGTA AAATGTTTTG AAGTTTATCA GAACTAAAT GTACTTTTAA AACGTATAGG 60
 GTCAGGGTTG GGGGAAAAAT ACAGGTATAG TAAGNAAGAA AAGTGACCCA TGAAGAAAGC 120
 ATCGTGAGGT TGTATGTTGG TTGACTGTGA TTAATATGCG GGGCTGGTGT AAGTTGTAAG 180
 TGGTGCTGA TTGCCGTGTA ACTATGTACA TGATTGTTGG GATGGCTGTC CCATATTTTG 240
 TATATTGGAA TAAAAATTTT TATAANTTAT NGTAACTAAA AGTAAATATT CTAAATTAAG 300
 TCCCACTNCT TAAGTCACAT GGCTTCTGTC TTGGGAATTT TACCTTTTAA NANGATTATT 360
 TTNAGN 366

SEQ ID NO:7367

SEQUENCE LENGTH:378

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08608

SEQUENCE DESCRIPTION:

GATCTTGGCT GTTCTTTCTA TTCTGCCAGC CATCTTCCAA AAAAACTAA AGCAGAAATT 60
 TGAGTAAAAA TAATCATCTG ATTTTAAGTT TTGCTGTCAT CACCATCTCA GGATTAACAG 120
 CTGCGACTTT AGGTGGGGTA TATTTCTTC TCCTAAGAGA ATAGACAGTT TTTCCAGATT 180
 CATCATCATT GACTGTCAAG AAAGGACCCT TCAGCAAGGC TGTACNTCA ATGCAGTTGA 240
 TGGCCTGTNT TCACGGNTTT ACAGACTTGG CCTGATGCCC ATGTAANTTC AAGCTTTGGC 300
 TTGTGGNAAC AACCACANGG ANGNCAAGGC ATCTGTNGGT GCGGGNGGGC AAAGCAGGCT 360
 TANCTNGGGN GGTGACN 378

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SEQ ID NO:7368

SEQUENCE LENGTH:421

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08609

SEQUENCE DESCRIPTION:

GATCTAGAAA CCCTTTTACC TGGCCCCAAG GCTCTAGCCA GTGGTCTCTG GTGACCCCTG 60
 CAAGCTCAGA GATGGGGNTG TTGTGTGCCA GGCATGAGCT TCCCCAAGAG GCAGAGGGCA 120
 TACATCCCAT TTATACATTC CCTAAGCCCA CCCCTGTNTC CTCAGGCACC ACCTGCCCTG 180
 GTCAGCTCCA GCCAGTCCCT GCTGGAGTGG TGCCAGGAAG TNACCACTGG CTACCGTGGG 240
 GTCCGAATCA CCAACTTNAC CACATNNTGG CGCAACGGCT TGGCCTTCTG TGCCATCCTG 300
 CACNGATTNT ACCCAGACAA GATGTGAGCT GCCAGAGGGG TGGGACGAAT GGGGGAGCCA 360
 TCAGGGAGGG CAGTNTGGAC CCAGCTTTGA CCAGANAATT TTTNGAGTGC TTTGCTNGTT 420
 N 421

SEQ ID NO:7369

SEQUENCE LENGTH:189

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08610

SEQUENCE DESCRIPTION:

GATCAGCAAT GAGTCGGCAA TTGACTTCTA CAGGAAGTTT GGCTTTGAGA TTATTGAGAC 60
 AAAGAAGAAC TACTATAAGA GGATAGAGCC CGCAGATGCT CATGTGCTGC AGAAAAACCT 120
 CAAAGTTCCT NCTGGTAAGA CNNCAGNTGT NAAAANGCCA GCAACCTGNC CAATTTCAN 180
 TGANCCTTN 189

SEQ ID NO:7370

SEQUENCE LENGTH:147

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08611

SEQUENCE DESCRIPTION:

GATCTGGTGG AGAAAAGAAG CAAAACCTTG TTTTAATTGA CTGTTTTTTT AAAATCTTTT 60
 TGGATATTGT TTTGCATCCC ATACATTTGC AACTGGCAAT GAAATGTAAG CTTTGGTTCT 120
 GAAAAAAAT AAATGTAGCT ATTCAAA 147

SEQ ID NO:7371

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08612

SEQUENCE DESCRIPTION:

GATCCACATG CNTGTGGCAG CCCAAGGCTT TGTGTAGGA GCAATGACTN TTGGTATGGN 60
 CTATNCCATG TATCGGGAAT NCTGGGCAAA ACCTAAGCCT TAGAAGAN 108

SEQ ID NO:7372

SEQUENCE LENGTH:273

SEQUENCE TYPE:nucleic acid

5 TOPOLOGY:linear

CLONE:HUMGS08613

SEQUENCE DESCRIPTION:

10 GATCTTTGAG CTGTGGTTTC TCCACCTGTG GAATATAAAT GTNAACAACA TAACCTTCTT 60
TCTAAGGATA ACTTGAGAAT TAACAGTGCA AGTAAATGGA AAGTATAGTA CCTGTNACCA 120
GATATTTAAT AGTAGTTATT ACGAAATTGT AACTCACTAC CTGTNTTAGT TGAGGTTTAT 180
CTTCAGCCAT GCAAATCAAA ATCAGATTAT TTNCACATCA GCAGATAAGG TTTGTNTGAG 240
ANTCTNATTT TNNATTTGNT ACTCTNATTT NNN 273

15 SEQ ID NO:7373

SEQUENCE LENGTH:419

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

20 CLONE:HUMGS08614

SEQUENCE DESCRIPTION:

25 GATCACAGAT GTAGTTCCTG AGGTTGAGTC TCCTTCTCAG ATGGATGTTG AATTGGTGAG 60
TGGGTCTCCT GTGGCACTCT CACCCAGGCC TCGATGTGTG AGGTCTGGTT GTNAGAAGCC 120
TCCCATTGTG AGTAAGGACT GGGACAATGA ATACTGCAGC AATGAGTGTG TGGTGAAGCA 180
CTGCAGGGAT GTATTCTTGG CCTGGGTAGC CTCTAGAAAT TCAAACACAG TGGTGTGTTGT 240
NAAATAGTCC TTCCTGTTCT CCAAGCCAGT GAAGAGTTAT CTGCTGGGAA AGTGTCGAAG 300
AGCCTGTTTT TGAACACAA GCTGGGCTTC TGGTAGTGCC TCATCACAAAC CCATGATGGC 360
TGTTTCATGGT TTCACCCCTT TTNTTTCNT CAGCAGAGGC CAGGCTATTG GAGCAGTTN 419

30 SEQ ID NO:7374

SEQUENCE LENGTH:209

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

35 CLONE:HUMGS08615

SEQUENCE DESCRIPTION:

40 GATCCTAATT TGCACACTAT CACCTAAAGT CCTAGCATACTGTCATTTC AGGAAATCTA 60
ATGAGAAAAGA AGTCCTGAAA GCCTCTAATT CCTGGAAACA TATGAAACGG CTAGAAAAAA 120
GTAGACTATT TTGGAGGATT AAAGACAATG GAAACTTTTT ACATTGTTTG TCTCACATAA 180
TGAATAAAAT TCCACTTTAA AAAATGAAA 209

SEQ ID NO:7375

SEQUENCE LENGTH:422

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08616

SEQUENCE DESCRIPTION:

50 GATCCGCAGC TCGAAAAAGA ACAAGCCACA GAANCGGGCT CGCTCGTGCC AGGACACAGC 60
AGTGTCTTTA AAAAAATCAA AACCAGAAGT TTTATCAGCA GCAGGAAGNN TGTGGGACTC 120

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5 TGTCCAAGTT CACCGTCACC ATCAAGCCAC TGGCTGTGGA AGGAGTTTNT CCAACAGGGT 180
 CAGTGTACACA GCCACAACCT CAGAAAGCAG CCATCCCGCG TGTCGTCCAA ACAGCAGTGC 240
 CTGCTTCCCG CTCCACGGAG TGTTCNGAA CACCTCCCTC TGAACATACT CCGGAGCACC 300
 CCACCCCCAG CGAGTCCAC CTGGACCTNT TCAAAGTCAA AACTCTTCTT TNGGGCCAAC 360
 CAATTNTTCG GGCTTTNGAG GCCTTGAAC TGGGGCACCA AGTTTNTTC CATGGGAANT 420
 TN 422

10 SEQ ID NO:7376
 SEQUENCE LENGTH:413
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08617

15 SEQUENCE DESCRIPTION:
 GATCCACCA GTTCTGGAC GTGGAGATC TGGGGCATCT CCTTCTTATG CCAAGGGGCG 60
 CTTNNNGTTT TCATGGCTGC CCCTCCAGAC TGCAGAAAC AAGTAAAAAC CCATTGGGGC 120
 CTCTTGATGT CTGGNATGGC ACGTGGCCCG ACCTCCACAA GCTCCCTCAT GCTTCCTGTC 180
 CCCCCTTAC ACGACAACGG GCCAGACCAC GGGAAAGGACG GTGTTGTNT CTGAGGGAGC 240
 20 TGCTGGCCAC AGTGAACACC CACGTTTATT CCTGCCTGCT CCGGCCAGGA CTGAACCCCT 300
 TCTCCACACC TGAACAGTTG GCTCAAGGGC CACCAGAAGC ATTTNTTAT TATTATTATT 360
 TTTTAACCTG GACATGCATT AAAGGGTCTA TTAGCTTTCA GAAAAAAAAA ATN 413

25 SEQ ID NO:7377
 SEQUENCE LENGTH:157
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08618

30 SEQUENCE DESCRIPTION:
 GATCCACAAA TGAAAGGGAT ATAAAAATAA TGTCATAGGT AAGAAACACA GCAACAATGA 60
 CTTAACCATA TAAATGTGGA GGCTATCAAC AAAGAATGGG CTGAAACAT TATAAANTT 120
 GACAATGATT TATTAAATAT GTTNTCTCAA TTGTAAA 157

35 SEQ ID NO:7378
 SEQUENCE LENGTH:399
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 40 CLONE:HUMGS08619

SEQUENCE DESCRIPTION:
 GATCCTAACA GCTTGCATTA TTTGGTGCAT CTGCTCAATC AAGTCTAATA GACACAAGGA 60
 TGGCTTTCAT CGGCTCAGGC AGCATCATGA TGAGTATGAA GATGNAATTC GCATGATGTC 120
 45 TACCGGCTCC AAGAAGTCCC TCCTAAGCCA TGAGTCCAG GATGAAACAG AACTGAAGA 180
 GGAAACATTA TATTCTAGCA AACATTGGNG GNCACATTTT GCATATCTCC CAGCATAAGT 240
 ACCAAGCAAA ATTACAGTTC CTCTTGGGAG AACACTGCAT TAAGGATGCG AGACTCTCTT 300
 GCTTCTTCAA AGNGCTTTTG GGAATTTAAA TTGCTAANTA TGTATTCTCA AAANAANNNN 360
 NGGGANNTT GGGGGGNTG GGTTTNCGG AGNGANGNN 399

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SEQ ID NO:7379
 SEQUENCE LENGTH:34
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08620
 SEQUENCE DESCRIPTION:
 GATCGGTCCC TAAACCTCAT TAAAATATTT GAAA 34

SEQ ID NO:7380
 SEQUENCE LENGTH:405
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08621
 SEQUENCE DESCRIPTION:
 GATCTNATGG ATATGGCAGT GGACGTGGAT TTGGGGATGG CTATAATGGG NATGGAGGAG 60
 GACCTGGAGG TGGCAATTTT GGAGGTAGCC CCGNTTATGG AGGAGGAAGA GGAGGATATG 120
 GTGGTGGAGG ACCTGGATAT GGCAACCAGG GTGGGGNCTA CGGAGGTNGT TATGACAACT 180
 ATGGAGGAGG AAATNATGGA AGTGGAAATT ACAATNATTT TNGAAATTAT ANCCAGCAAC 240
 CTTCTAACTA CGGTCCAATG TNGAGTGGAA ACTTTGGTGG TAGCAGGAAC ATGGGGGNAC 300
 CATATGGTGG AGGAAACTAT GGTCCAGNAG GCAGTNGAGG AAGTNGGGGT TATTGTNGGA 360
 NGNGGCCGAT ACTGAGCTTC CTTCTATTT NNCCATGGCA TTTNN 405

SEQ ID NO:7381
 SEQUENCE LENGTH:261
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08622
 SEQUENCE DESCRIPTION:
 GATCCTAGCC AGATTACCAG AAATTNCGTT AGTCATCTAA ATCAGAGACA TCAATTTNAT 60
 TATGGAGAAT TTNTGAATCT CCAGCTAGAT GANGAAACCC AATACCAAAC TCCTGTTGAA 120
 GAATCTTTNC AAGTAAACAT CTGAAGGCTG TAGACATCTC TCCATCTTTG TACCTGCAAG 180
 TCCCATCTTT AAGGGGGAAA CTACATGANG TCACCGTTAC AGTAACTTGA TGTGTATATT 240
 AATAAAAGTA ATTCAGTCAA A 261

SEQ ID NO:7382
 SEQUENCE LENGTH:44
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08623
 SEQUENCE DESCRIPTION:
 GATCTATGTA TAGATAAAGA TTAACATAT CTAGTACAAG GAAA 44

SEQ ID NO:7383
 SEQUENCE LENGTH:109
 SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear

CLONE:HUMGS08624

SEQUENCE DESCRIPTION:

5 GATCTGTTTC TTAAAGCTAC AGGGTTTAAA AAATAAAAAAT GAGTGAAAAAT ACTTGATGTT 60
TCTTGAAAGA TAAATTTAAT AATAATAAAT AAATACATAA ATACATAAA 109

SEQ ID NO:7384

10 SEQUENCE LENGTH:93

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08625

SEQUENCE DESCRIPTION:

15 GATCATTGTG GCGTCCACAA TGTATATATA AAACAAGTTG TACACATTAC CATGTATAAA 60
TTTGTGTTTG TCGATTATAT GTCAAGAAAAG AAA 93

SEQ ID NO:7385

20 SEQUENCE LENGTH:54

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08626

SEQUENCE DESCRIPTION:

25 GATCTTAATC TTATTCTCTG CCATCTTCAA ATTAAAAAAA AATTTCTTTG TAAA 54

SEQ ID NO:7386

SEQUENCE LENGTH:140

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08627

SEQUENCE DESCRIPTION:

35 GATCCCTTCA GAAGAAGACA TGATAGGATT GTAAGTTTTT NTCTAACTTT GGATGCAGTG 60
AGATGACCAG TGTGTTCCAG TTAAAGAAGA AGAGTGTTTT AAAATCATAA ACCAAATAAA 120
GAATCCTACC TTACATTAAA 140

SEQ ID NO:7387

40 SEQUENCE LENGTH:206

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08628

SEQUENCE DESCRIPTION:

45 GATCCACCCA CCTCAGCCTC CCAAAGTGCT GGGATTACAA GCGTGANCAC TGTGCCTGGC 60
CCTTTTTTTT TTNAAGAGA TGGCATCTTG CTATGTCGTC CAGGCTGGTN TTGAACTCCT 120
GAGTTCAAGC AGTCCTCCTG NTTCAACATA CAGNTACAGG TACCCCCCAC TATACATTTT 180
NAATANGGNT TCATGGNTCA GNGGGN 206

50 SEQ ID NO:7388

55

EP 0 679 716 A1

SEQUENCE LENGTH:130

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08629

SEQUENCE DESCRIPTION:

GATCCCATTTG CTTTCCTGTT TTAATAATAT TTTATGCTCT TTATTTCCAC TTCTGTGAAT 60
GTGATATTTT TATTTTNTGA TTATGTTACT GAATAAACAA ACTTGCTACA TAAATNCTT 120
AGCAATTAAA 130

SEQ ID NO:7389

SEQUENCE LENGTH:355

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08630

SEQUENCE DESCRIPTION:

GATCCAATTG TGGATTTATT TACAAACATC AAATGCCTTC AAGCCAATCC TTTTGCTGT 60
ATGTTTTGCA GCCTACTGTA GTAGATACGC AACAGATAAT GTGGGAAAAA AAGAGATAAG 120
AGGAGGAAGC TAATAAGAGA CTGTCAAGAT TGTATACCTT CTTGGTTTCT TTTAAGAATT 180
TGTTCCTTT NTACTATNNC AGCAAAGCAG CATTTTGTGA CTGACTGCCT AAAATCACTT 240
AATCTCAGGT GAACGCATCA CTTGCCAAAC TGTTGGAATG CTATTGTGT TTTGTTGCAC 300
TGTTTTTTC GTTGTGTGT TTGTTATTT GGTGGCTTT TTGGAGAGGG AAATN 355

SEQ ID NO:7390

SEQUENCE LENGTH:96

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08631

SEQUENCE DESCRIPTION:

GATCTAAAT NAGAGAAGCA TTTAAAAAT NATTTCTGTC TTGGTTCATC TTATTGTTAG 60
TGGTTTATGC TAATAAAAT TGATTAAACA ATCAAA 96

SEQ ID NO:7391

SEQUENCE LENGTH:411

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08632

SEQUENCE DESCRIPTION:

GATCCAGATA TGTCTGTTAT GAAAGATATC AGTATAGGTA AAGCCACAGG CAGAGGTCAG 60
TACTGATAAT TAATGTAGTA TAAATACATC ATTTACCATT TTATTTTAAA TAGGAAGCCA 120
TCAAGCATGC TAGAATTGTG AACTTTCATT ATATNTTTT GTTGTGACA TGAATTAACC 180
TGGCCAAAAA CAAAAAAGAA NNAAAAAACC ATGCCATTG TCATGTAAAC CTTTTTTT 240
TCCCTATGGG CCTTNGGGN CNGAATCAGT ACTTCAGTTA TTGTAATNGT GNGCTAACCT 300
CAAATTTN TN TCACCCNGTT GCCCTTTTCA TGNCCTAACC AATTNTCTGG GGGNTTGGTA 360
TGGTTCNCCC GGTCTGNTC ATGTTACCG NNCTCTTTT TNGNGGGTCC N 411

SEQ ID NO:7392

SEQUENCE LENGTH:248

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08633

SEQUENCE DESCRIPTION:

GATCTAAGTT CTAAGCCAAA TAACTAACAA ATTCCAGGTA CTATGCCATC ATATAATATT 60
 TATAAATGTG TTATATATAT TATGAGATAT GTATAAGAAT ATAGAATGAA TATGTAATAA 120
 ATTATACTTT TAAATTAATA TTTTCAAATA TATAAATATG TAGTTTCAGA CTGAAACTGT 180
 TCTAAACTAT ATAAATGTAT TATGTATGTT TTATAAATA CAGTACTCAT AATATGTATT 240
 ATATGAAA 248

SEQ ID NO:7393

SEQUENCE LENGTH:247

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08634

SEQUENCE DESCRIPTION:

GATCCTTCCA CCTCAGCCTC CCCAGTAGCT GGGACTACGG GGTCGCCACT GCACCCAGCC 60
 TGTGTCTTCC AGCTCTAATC AGAAAGCTGC TTGTCGAGGG CATGGGGAAT CAAACTGAAT 120
 GAACTTTTCT CTGCACTGTG GCAAACTGT TATTTTATG GATTTTACTA AATGGCGTTA 180
 CCTTTTCAAG ATTTATATGT TTGTATAATC ATAAGAAAAT TGAGCCATTA AAGCCTTGTT 240
 ATTCAAA 247

SEQ ID NO:7394

SEQUENCE LENGTH:108

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08635

SEQUENCE DESCRIPTION:

GATCCAGGCT CGTAGNTCAC TCCCTGCCCG TNTCCAGAG ATGCTTCACC ANCACCTGCC 60
 TCTGAGACCT CGCTCTCTGT TCCAGCAACC CTGGNTTGGG GGGTCANN 108

SEQ ID NO:7395

SEQUENCE LENGTH:61

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08636

SEQUENCE DESCRIPTION:

GATCTTGAGC TCCTGGCCTC CAGAATTGCA GGAGAATAAA TNTGTGTTGT TTTTAATGAA 60
 A 61

SEQ ID NO:7396

SEQUENCE LENGTH:275

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08637

SEQUENCE DESCRIPTION:

5 GATCAGTGTT TGNTTGGGAC TGAAGGGATG ACTAATAAGG AGCAGAGGAA AGCTTTTGGG 60
 GATGATGGCA CTCTTCTCTG TCTCCATTAC GGCATTGGAT ACAAGTCTCT AGAACTCCCA 120
 GAACTCGTCA CTGAAAGGGG TGAATAGTAC TGTATGTAAA TTAGGTCCNN ATTTTNAAAT 180
 GGGANAAATA AATATAAAGA CAAATTACAC TGCTGTATTA NNTCANNTGA TAGATGTAAA 240
 10 AGTCTAATAT ATACGTNTTT TTCNTGATAN NCCCN 275

SEQ ID NO:7397

SEQUENCE LENGTH:288

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS08638

SEQUENCE DESCRIPTION:

20 GATCCACGCC CTCCCCGCA GTCTGGAGAG GGCCCTGACC GAGGACTCAA CCCAAACCAG 60
 TGACACAGCT ACCAATTCTA CTTTACCTTC TGCAGAGGTG GCGTTACAGG CAAAGTGAGG 120
 AGGGAGCTGG GGGACACTTT CGAGCTCCCA GCTCCAGCTT CGTCTCACCT TGAGTTAGGC 180
 TGAGCCACAG GCATTTCTTG CTTATTTTAG GATTACCCAC TCATCAGAAA AAAAAAAG 240
 GCCTTTGTGN CCCNTGTTTT GGGGGGATTA ACCNGTTTTG GGTTTAAA 288

25 SEQ ID NO:7398

SEQUENCE LENGTH:290

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

30 CLONE:HUMGS08639

SEQUENCE DESCRIPTION:

35 GATCTAATTN CTATTTCAAT TATTCAGAAA TAGCATTTAG ACATAAAANC CAATGTCTCA 60
 CTTTGTAATAA TAACCTTTGG CTAATTTACA CACATCTAAT ACAGCGTGTT ATATAAGTTT 120
 TAAGTAATAC AATGAGTCAC TACTATCATT CAGTTTAAAN TATTTNNGT GTTAACAGGG 180
 CTGAGAATAT CATGTGGTTC AGTCTTCTGN NGGNCGTAT ATNATACCNG CNTAGTGCCT 240
 TTGACCATGC NACTATCCT CAAGGCCAGA CATCCTACAN CGGAAGTGN 290

SEQ ID NO:7399

SEQUENCE LENGTH:267

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08640

SEQUENCE DESCRIPTION:

45 GATCCNTAAG TACTCTTCTC TANAGAATAA AATGCATTAC CTAGGCTTTA ATAGTTAAAA 60
 GCTGGNATTT ATNGACCCGC ATCTACTTGA TTTCANAATA TGCATTGATT TTAGTATGTT 120
 GCTGNTCTGT TATCTGTACT CAACTATANC AGAGTAATAT ATTGTGGTNT TCTGGACCAA 180
 AANTCGTGCT ACACATATGT CTGATGGCCT TNACCTTTTC ANGACAACAG TTGCAATTTT 240
 50 GAGCACAGTC CNCCTAGTGG TANTCTN 267

55

SEQ ID NO:7400

SEQUENCE LENGTH:127

SEQUENCE TYPE:nucleic acid

5 TOPOLOGY:linear

CLONE:HUMGS08641

SEQUENCE DESCRIPTION:

10 GATCGGGAGC AGCCCCACTG GACCTAGGTG CCCCATCTGT TGGTCATCCA TCCTGAAGGG 60
ACAGGAAACC TCCCAGGCAG TTATTTTTTT TTCTCTATAT TTCTAGTAAA GTTTTCGATA 120
TGTTAAA 127

SEQ ID NO:7401

SEQUENCE LENGTH:168

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08642

SEQUENCE DESCRIPTION:

20 GATCACTAGT GCAGGAGAAC ATTACATTTT CTTCTGAAGG CAAAATGCTT GTAGGTTTTG 60
CCTCTACTTT GTATTTACTT TAAAAATTGC ACTTGTTTAC CTACCAGTGT TTACGAAATC 120
CTGTATTGG GATGCTTTTT CTATAATAAA ATATTATAAT TTGTGAAA 168

SEQ ID NO:7402

25 SEQUENCE LENGTH:323

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08643

SEQUENCE DESCRIPTION:

30 GATCATAGTA AAGAGTAGTC AATAGGGTCT TCAGCTATTA ATTGTAGAGG TGATTAAAAC 60
CAACAAGGAG TTTCATGTGC AAAGGAGATA AGGAATGAAT ATAAAGATTG CTATTGGGGT 120
GGCTCTTATT AAAGTGTGTA TTTTGTACTT ATCACTACAC GTATCCCCCA AATGCTTACA 180
TGGGAGTTTG AGGTTAGTAT TTTCACCTCC TTGGTGTTAG TACTCTATTC ACATTCTTAT 240
35 TGTAACCTTC CTCATTTCAC AGATAAGGAA TCTTTGGGGA TTAACCAACC TCCTTTCTGT 300
AATGGTAATC ATTAAANTAA GTN 323

SEQ ID NO:7403

SEQUENCE LENGTH:94

40 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08644

SEQUENCE DESCRIPTION:

45 GATCACTTAN GCCCAGGAGG CAGAGGTCAC AATGAGCCGA AATTGTGCCA ACTGCACTCC 60
AGCCTGGGCA ACAGAGGAAG ACTCTTCACA GAAA 94

SEQ ID NO:7404

SEQUENCE LENGTH:226

50 SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS08645

SEQUENCE DESCRIPTION:

5 GATCGGGGCT TTGTGTTTAA CCTCATCAGA CATTATTGCA GCCAGCTGTC AGCCAAGCTC 60
 AGTAACCTTC CAACGCTCAT TTCCATGAGG CTAGAGTTCC TGAGAATCCT CTGTAGCCAT 120
 GAGCATTACC TCAATCTGAA CCTTTTTTTT ATGAATGCTG ATACTGNTCC NACATCTCCT 180
 TGCCTTCCA TATCTTCCA GGTAATAAAA GAATTATTTA ACTAAA 226

10

SEQ ID NO:7405

SEQUENCE LENGTH:124

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

15

CLONE:HUMGS08646

SEQUENCE DESCRIPTION:

GATCCAGTCA GAGCCAGGGA GAGTGTTCCT CTTAAGGAGG GACTCCCTTG TCCAGGATGG 60
 GGCTGGCACT AGGGATGGGG TGAATCTTAG GACAGGAGTG GGGGTCAGAA ATGGGAGGGG 120
 TAAA 124

20

SEQ ID NO:7406

SEQUENCE LENGTH:206

SEQUENCE TYPE:nucleic acid

25

TOPOLOGY:linear

CLONE:HUMGS08647

SEQUENCE DESCRIPTION:

30 GATCGACCAG CAGGTGGTCT ATATCCATCC TTCCAGTGCC CTCTTCAACA GACAGCCAGA 60
 ATGCCAAAAG AACTTCCTCC CTNTGGTTGC TGTAGGTGTC TCATTGGAGC AGTGCCTCTC 120
 CAAGTTTGAG GATNTGAACA AAGAACTGGG ACTGGTGACT TGTNANNGNN NAGTTCAGAG 180
 GGCAGAGGNC CATCATCTCA GCTTNN 206

35

SEQ ID NO:7407

SEQUENCE LENGTH:103

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08648

SEQUENCE DESCRIPTION:

40 GATCCATAAG GAGGGCTGTG TGGNGAAGAT TCAGGGACTG ANTAGAGGGA AAATCGTGCT 60
 ATNCGGTAGC TACAGCAGCC CTGGGAATNC CNTTTTGTCT AGN 103

45

SEQ ID NO:7408

SEQUENCE LENGTH:116

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08649

SEQUENCE DESCRIPTION:

50 GATCCATAAG NAGGGCTGTG TGGAGAAGAT TCGGGNCTGG CTGAGGAAAA ANCGGCTGGT 60

55

GGTAGCTACA GCANCCCTTG GAATACCCCTT TTGTCGAGGT TTTGGGNATT GTCTCN 116

SEQ ID NO:7409

SEQUENCE LENGTH:60

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08650

SEQUENCE DESCRIPTION:

GATCTATCAT GTATCTTGGT GATTACAGTT AATAATATAT TGTATATTG ANAATNGAAA 60

SEQ ID NO:7410

SEQUENCE LENGTH:91

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08651

SEQUENCE DESCRIPTION:

GATCGCACCA CCGCACTCCA GCCTGGGCAA CAGAGCAAGA CTGTTTCAAA ATAAATAAAT 60
AAAATAATAA ATAANNCTTT CCAACTNCAA A 91

SEQ ID NO:7411

SEQUENCE LENGTH:240

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08652

SEQUENCE DESCRIPTION:

GATCTTGTGG CTAAACCAGC ATTTCTGTGT TTGAGAGATT TCCTGTTAGG TGCTTCGTCT 60
GAAAGTGAAC TCTCATAATT CAAATTGTAT AAANTAAAGC TACATTTCTA AGAGCTTGGT 120
GTAGGGCAAT TGAATANTG TCCTGTTAGA TAAACAGACA TTTAGCANTC CTGACATTAA 180
AAGGAAATGT ATTTCTATAC AGGATTATTA GCTGTANTAC ANGATATTTA TTTANCCAAA 240

SEQ ID NO:7412

SEQUENCE LENGTH:247

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08653

SEQUENCE DESCRIPTION:

GATCGCACCA CTGAACTCCA GCCCGNATGA CAGAGTGAGA CCCTGTTTCT AAAACAAAA 60
CAAACAAACA AACAAACAAC GTATCTTACT GACTAACTG GAATGGAAAT CTTATAATNA 120
GTGTTGTATT TTTCTGCAAA ATAGTGAATT NGNACTTGGG AGACTTCNNN NCTTTGTTGA 180
AAAAAATTGC CTTTGTTTTG AAATTATATC ACCTGTGTTC TGANCTAAAA TGNTGGGAGT 240
TCATNNN 247

SEQ ID NO:7413

SEQUENCE LENGTH:128

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08654

SEQUENCE DESCRIPTION:

5 GATCCATAAG GAGGGCTGTG TGGAGAAGAT TCAGGNANCT GACTGAGGAA AAATNTGCTG 60
GTGGTAGNTA CAGCANCCCT TGGAAATACC TTTGTGCGAA AAATAAAGGA ATTGTCTTCA 120
NCCTGCTN 128

SEQ ID NO:7414

SEQUENCE LENGTH:118

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08655

SEQUENCE DESCRIPTION:

15 GATCCATAAG NAGGGCTGTG TGGAGAAGAT TCAGGGAGCT GACTANAGGA AAAATGTGCT 60
GGTGGNANAT ACAGCAACCC TTGGAATANC CTTTGTGCGA GAATAAAGGA ATTGTCTN 118

SEQ ID NO:7415

SEQUENCE LENGTH:151

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08656

SEQUENCE DESCRIPTION:

25 GATCTTTNTN ATATATGCAG TCCCATCCCT TCTGTGCCAC TCAATGCCAT CCAGACATGG 60
TTTNCCTC CANGGGCCTT TCTCTCCAGA GGGCACTCG GCTGCCTCTG CTTCTCTCA 120
TTCGAGGCC GNCTCTNCT NACAGAATAG N 151

SEQ ID NO:7416

SEQUENCE LENGTH:374

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08657

SEQUENCE DESCRIPTION:

35 GATCCC GTTG CCTCATGGAA CTCATGCATT TCACGCTGCT TGCCCTTTCT GTGCTACACA 60
GCTGGTTGGG GNGCAAACT GCATCAAATT AATTNCCAA GGTCCAATTG ACTGACGCCC 120
40 TTGACAGCCA TCTACGACTT TATTAACAGG TTAGTGTGAA GATTTNCCA CTAACCTTAG 180
ATTTNCCTT TTTGTAATGC TGTTTATCAG AGGCGGGTGA CANGGGCTGG AAATAAAGNG 240
AGGGGACATG GTGATGAAAC ATGGCAGGNG TGTACAGATA CCAGTGGTGT GTTGCATGCT 300
CAANACAGCA GCGTCGTCAA TGGCGTCTGC TTGNTGNNC CATNATGTCT TTGTCATAAT 360
TGGNAANNAA NNNN 374

SEQ ID NO:7417

SEQUENCE LENGTH:110

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08658

SEQUENCE DESCRIPTION:

GATCTTTATG TCACTAGTTA TAGTTAAGTT CATTGAGACA TAATTATATA AAAACTACGT 60
GGATGTACCG TCATTTGAGG ACTTGCTTAC TAAAACTACA AACTTCAAA 110

SEQ ID NO:7418

SEQUENCE LENGTH:232

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08659

SEQUENCE DESCRIPTION:

GATCTTTTTA ATTCACTACA ATCTCTGAAG GTGTTAACAC TAATNTTTTA CAAGAATGTA 60
GAGGCGACTC GGTGCTATGA AGCGTGTTAA ACAACTCACA CAATTGCTAC AAAACACCAG 120
GGAGGGGCTT TTTGTGTTTT TAATTTTAA AACATTTTTC CTTTCTTGT GAGCCATAGT 180
AGGCCTAGAG AGATTACTGG GTTTTATAA TTAAACATTT ATTCGGTGA AA 232

SEQ ID NO:7419

SEQUENCE LENGTH:370

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08660

SEQUENCE DESCRIPTION:

GATCTTAACC AGTCGAGTGG AGTGTACATT GTCTGAATAC AGGATGCACA ATGTTGTCAA 60
TCCTGGAAAT GGTCTTTCTT TTTTGTAAGA TATGTGAATG AAGTGTTGGT GTCCTCACCA 120
AGAGGTGGCA CTAAGGGTT CTGAGGAAAT AAATGTATAG ACCCTTATGT ACAGACCTGT 180
GTATAANCAN CTNNGTATA TACATATAAG GATAGCTTTT TTGACCTATA CAGCTGTNCA 240
TAAAAGTAGC TGATATTAGT TAGGCCTGTG TCACCAGTTT GGNTTTTTTN CACTGGTNCA 300
TTTGGGATTT NNTTTTNGGT GGTTTAAAT GGCATATGCT AAGGTGTGTG ATTGGGAANA 360
AANNANNANN 370

SEQ ID NO:7420

SEQUENCE LENGTH:83

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08661

SEQUENCE DESCRIPTION:

GATCTGTGTT TTAATGAGTT TCACAGTGTG ATTTTGATTA TNAATTGTGC AAGCTTTTCC 60
TAATAAACGT GGAGAATCAC AAA 83

SEQ ID NO:7421

SEQUENCE LENGTH:394

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08662

SEQUENCE DESCRIPTION:

GATCCTCTCT TACCCCGTCC CCAGGTTTGA AACACATAGC CTCATTTCAA GGTGTAGCCA 60

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GGTTCCTCCG ACTTTCCTCT GGGATATAAA AAAGGGGGTA AGGGGGCAAA GAGAGCCCTC 120
 TGGGACTCTC CTCCCATACA CACTACACTG CCCCTTCTCC CCCCATCAAA ACGCTCAGNG 180
 ACGTTGTGAT GATGCGACTG AGGATTATGC AACGTGGTCC AACCGGAGCG GNCAGCATGA 240
 CCAGCTGTCC AGGGGCTGNC TNCTGCCCTT TCTTTTGTA AAGCCANGAC CCTTGGGGAG 300
 TTTTAATNCT GTTTGTACT TGNCTGTGG GGNCTNCACT TGCTTTTCT ATGGGAGACA 360
 CTTTNAAT TTAACAAGNT GNGGGTTTT TGNN 394

SEQ ID NO:7422

SEQUENCE LENGTH:134

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08663

SEQUENCE DESCRIPTION:

GATCCCCATG CCTGAGGCC CCTCGGCTGG CCTGGGCATG TGATGGCTCC TCACTGGGAG 60
 CCTGTGGGGG AGGCTCAGGT GTCTGGAGGG GGTGTGTGCC TGATAACGTA ATAACACCAG 120
 TGGAGACTTG CAAA 134

SEQ ID NO:7423

SEQUENCE LENGTH:69

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08664

SEQUENCE DESCRIPTION:

GATCATGNGT TTCCTCATGA GGACAAATAC CTGATTTTGA ATAAAGCAGC ATTCAGTTGA 60
 AATAACAAA 69

SEQ ID NO:7424

SEQUENCE LENGTH:52

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08665

SEQUENCE DESCRIPTION:

GATCAACATT TTTTAAAAA GAGCATTAAA GAAAGAATTG TGGTACAATA AA 52

SEQ ID NO:7425

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08666

SEQUENCE DESCRIPTION:

GATCACACAT TCAGACTGTT GTGTCTGTGG AGTTTTAGGA GTGGGGGGTG ACCTTTCTGG 60
 TCTTTGCACT TCCATCCTCT GCACTTCCA TCTGGCATCC CACGCGTTGT CCCCTGCACT 120
 TCTGGAAGGC ACAGGGTGTCT GCTGCCCTCT GGTCTTTGCC TTTGCTGGGC CTTCTGTGCA 180
 GGACGCTCAG CCTCAGGGCT CAGAAGGTGC CAGTCCGGTC CCAGGTCCCT TGTCCTTCC 240
 ACAGAGGCCT TCCTAGAAGA TGCATCTAGA GTGTCAGCCT TATCAGTGTT TAAGATTTTC 300

NTTNTATTTT TAATTTTTTT GAGACAGAAT CTCACTCTCT CGNCCAGGCT GGAGTN 356

SEQ ID NO:7426

SEQUENCE LENGTH:246

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08667

SEQUENCE DESCRIPTION:

GATCGTCGCC CCTCTGCCAA CTGCGACCCC TTTTCGGTGA CAGAAGCCCT CATCCGCACG 60

TGTCTTCTCA ATNAAACCGG CGATGAGCCC TTCNAGTACA AAAATTAAGT GGACTAGACC 120

TCCAGCTGTT GAGCCCTCC TAGTTCTTCA TCCCACTCCA ACTCTTCCCC CTCTCCCACT 180

TGTCCCGATT GTAACCAAA GGGTGAATA TCAAGGTCGT TTTTTCATT CCATGTGCCC 240

AGTAAA 246

SEQ ID NO:7427

SEQUENCE LENGTH:286

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08668

SEQUENCE DESCRIPTION:

GATCCTTGCA GGAACCTAAG GATTACAGCA GCTGCAGATG GCAGGAGCTA CAAGCCAGCA 60

GCAGCCAATG CTCANTGGGG TACAAATGGC TCAGGCAGGT CAACCAGGGA AAATGCCAAG 120

TGGAATAAAA ACCAACATCA AGTCGGCTTC CATGCATCCC TACCAGCGGT GAGTGTGGCT 180

GGCAACCTCG ACTCCCTGGT GCTCTTTGCA GAGTTGGGCA GTGAAATNNN NNNNTGCTCA 240

AGGCTCACCT AGGATGGGTA CAATAAAAAG AACATGGGCT TTCAA 286

SEQ ID NO:7428

SEQUENCE LENGTH:177

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08669

SEQUENCE DESCRIPTION:

GATCACTAAC AGGTGATGGG CTTTGTGCCC ACTCCAGAGA TATTGTGGGA GACAAATTCT 60

TTTAACAGCC TGTCTCCCG GCATCAGGAG TCATTGAACA ATCATGGATT GTTGTGTTTG 120

GGATTTTTTT TTTTNGGN TTNNTTTGG GTTTNGNGN GTGTGTGTGT GNCCTGN 177

SEQ ID NO:7429

SEQUENCE LENGTH:388

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08670

SEQUENCE DESCRIPTION:

GATCCAGGTG GTCCAGGAGC CCAGGACAGG CCTTINCTGT GGGCCCTGGC CAGACAGGGT 60

TACCTGGTGA GGTGCAGAGA GTCCCTCTAG TGGCCATTTT GTATGGTAGT TGCTAATGCA 120

GAACAAGTTC TGTCTGGGC TTAAATTGAC TGAAGACTTT AGGGGAAAG AATAGTAAAT 180

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GCATGTAAAC AAATGGGGAC ACTCTGTTCA GGAGAATAAT CCGACTGGCA TTTGTGGCAG 240
 TTTTGTAAAT GTAAATGTAT TCATGTGTGT TCTTGTAAT ACGTGTGCT CAGATGTCCT 300
 TTGAAGTGGG AGGGAATCAA TCCGGGGATA ATTTCAAATG GAATAGAGTA TTTTGATATT 360
 5 GTTCATTGAG AGGGTGATGT GTACACAN 388

SEQ ID NO:7430
 SEQUENCE LENGTH:392
 SEQUENCE TYPE:nucleic acid
 10 TOPOLOGY:linear
 CLONE:HUMGS08671
 SEQUENCE DESCRIPTION:
 GATCCCCACT GTCAATGGGG GATTGTCCCA GCCCCTCTTC CCTTCCCCTC ACCTGGAAGC 60
 15 TTCTTCAACC AATCCCTTCA CACTCTCTCC CCCATCCCCC CAAGATACAC ACTGGACCCT 120
 CTCTTGCTGA ATGTGGGCAT TAATTTTTTG ACTGCAGCTC TGCTTCTCCA GCCCCGCCGT 180
 GGGTGGCAAG CTGTGTTTCA ACCTAAATTT TCTGGAAGGG GACAGTGAAA AGAGGAGTGA 240
 CAGGAGGAAA AGGGGGAGAC AAAACTCCTA CTCTCAACCT CACACCAACA CCTCCCATTA 300
 20 TCACTCTCTC TGCCCNATT CCTTCAAGAG GAGACCCTTT GGGGACAAGG CCGTTTCTTT 360
 GTTCTGAGC ATAAAGAGGA AAATAAATCT TN 392

SEQ ID NO:7431
 SEQUENCE LENGTH:127
 25 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08673
 SEQUENCE DESCRIPTION:
 GATTTTGGG AAGGGAGACT AGGGCAGGTG GAGACAGCGC AGAACCCCGG TGCTGGGTGG 60
 30 GAAGCATGAC CACACGGTGG GTGAGCAGCC CCCATGCACT GATGGTAAAT TCCCCTGTGG 120
 ACTCAAA 127

SEQ ID NO:7432
 35 SEQUENCE LENGTH:353
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08674
 SEQUENCE DESCRIPTION:
 40 GATCTGTCTG GCATGTCAGG AGCCAGAGAT ATTTTATAT CAAAAATTGT CCACAAGTCA 60
 TTTGTGGAAG TGAATGAAGA GGGAAACAGAG GCGGCAGCTG CCACAGCAGG CATCGCAACT 120
 TTCTGCATGT TGATGCCCGA AGAAAAATTC ACTGCCGACC ATCCATTCTT TTTNNNNNTT 180
 CGGCATAATT CCTCAGGTAG CATCTATTG TTGGGGAGAT TTTCTTCCCC TTAGAAGAAA 240
 45 GAGACTGTAG CAATACAAAA ATCAAGCTTA GTGCTTTATT ACCTGAGTTT TTAATAGAG 300
 CCAATATGTC TTTATAANCT TTNCCCACT AAAACCCACT TGTCCCAAAG AAA 353

SEQ ID NO:7433
 SEQUENCE LENGTH:399
 50 SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS08675

SEQUENCE DESCRIPTION:

5 GATCTAATTG GCTTTTATTA GCAATTCATG AGCCCGGCAG CATCCAGTCT AAAAAATAGA 60
 AAGGAGTGCC ACTAAGCTAG ACAGAATGGA TGGGTTTAT GGCAGAAAA AGTGGGAAGCA 120
 AGCAAGAACA ATGAACAAAT TAATGGATGG ATTGTTTAA GATTACATTT CTTTATGGG 180
 AGTAAACAAA ATCTTGTTAG CCTAATGGAA TTTGGCATCA TCTCCTGATT TCTCAGAAGG 240
 10 TCATATCTTG TAAGTGAACC ATTTAGGTTT GGTGACCTGG NACCTTTGGC ATAANGTGAC 300
 TCCATTTTGG GGCCTGCTGC CTTTTCTTT AAAAANGGAG TGACACCNTA ATTTCCATGG 360
 GNNGAGCACA CANNATGCCC TTGTNTTGCA GGACCTNCN 399

SEQ ID NO:7434

15 SEQUENCE LENGTH:230

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08676

20 SEQUENCE DESCRIPTION:

GATCCTGACC ATATTCTCA AGGTCTCCTT TTCCTTCCTC CAGTGTAACA AAATTCCTG 60
 CTGGCGTCCT ATGTAAGAT AATCGGCCCT TTTGGACCT TTTGTTGGG TCAAGAATTT 120
 GGGTGGGAGA AAAGAAAGTG GGTATCAAG GGTGATTGA AATTTTCTGC AGCATTAAAG 180
 25 CTGGCGCTTA ATAAGAATAA GTAATAATAA AGAAATTCT AACATTCAAA 230

SEQ ID NO:7435

SEQUENCE LENGTH:153

SEQUENCE TYPE:nucleic acid

30 TOPOLOGY:linear

CLONE:HUMGS08677

SEQUENCE DESCRIPTION:

GATCCTGAAA ATAGCCCCGT GAAGGCAGAA ATGTATGTGA CTAGAACGAG GCCACATGAA 60
 TAAGCCACTG CCCACTGGCA GGAGTGAAAA CTGAAGCGCT CTTACCTGA AGGACCCCAA 120
 35 AACCATATAG AATAGAATAA CCAGGAGTTC AAA 153

SEQ ID NO:7436

SEQUENCE LENGTH:138

SEQUENCE TYPE:nucleic acid

40 TOPOLOGY:linear

CLONE:HUMGS08678

SEQUENCE DESCRIPTION:

GATCTCACAA GCNCTTTCCC TCTTGGTGCC TCAGTTTCCT GACCTATGAA ACAGAGAAAA 60
 45 TAAAAGCACT TATTTATTGT TGTGGAGGC TGCAAANTGT TAGTAGATAT GAGGCATTG 120
 CAGCTGTGCC ATATTAAT 138

SEQ ID NO:7437

SEQUENCE LENGTH:361

SEQUENCE TYPE:nucleic acid

EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS08679

SEQUENCE DESCRIPTION:

5 GATCATGGCT AAAGATGACC TCTCTGGTGC TGACATCAAG GCAATCTGTA CAGAAGCTGG 60
TCTGATGGCC TTAAGAGAAC GTAGAATGAA AGTAACAAAT GAAGACTTCA AAAAACTAA 120
AGAAAATNTT CTTTATAAGA AACAGGAAGG CACCCCTGAG GGGCTGTATC TCTAATGANC 180
CATGGCTGTC ATCAGGAAAA TGGTTGGGAG ATTTCTCAAT CCCTGAAAGG ATGAGGTTGG 240
GGGAGTTGCC CAGAGGAATC CCTGTTCCCA CTGATTTTAA TTAGCAAAAC ATCCTGTGTC 300
10 TTTTGGAGTA CGNTGTGTAA GTGCCCATG GGTGGCCTGT TNGGTCACTG TGCAGCAGTT 360
N 361

SEQ ID NO:7438

15 SEQUENCE LENGTH:273

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08680

SEQUENCE DESCRIPTION:

20 GATCAAGTG TAAACACCAT AGGGACCCNT TCTACACAGA GCAGGACTGC ACAGCGTCCT 60
GTCCACACCC AGCTCAGCAT TTCCACACCA AGCAGCAACA GCAAATNACG ACCACTGCTA 120
GATGTCTATT CTTGTTGGAG ACATGGGATG ATTATNNNCT GTTCTATTTG TGCTTAGTCC 180
AATTCCTTGC ACATAGTAGG NACCNNGTTC AATTACTATT GNATGAATTA AGAATTGGTT 240
25 GCCATAAAAA TAAATNNGGT TCATTTAANG TNN 273

SEQ ID NO:7439

SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

30 TOPOLOGY:linear

CLONE:HUMGS08681

SEQUENCE DESCRIPTION:

GATCAGAGGA ATGTTATNTT GTTCAGCCTT CTGGTTGGTT CACAGTAGTG ATAGTATTGT 60
35 AAATACTCAG AGCAATCCTA CAAGAAGAAA ACTACATNAG CCCCCACATG TTCCCCCCTAA 120
CATACCCCAT CACAGCAACT GAAAACAAGA GAAATGTTAG TTTTCTGTGG AAA 173

SEQ ID NO:7440

SEQUENCE LENGTH:194

SEQUENCE TYPE:nucleic acid

40 TOPOLOGY:linear

CLONE:HUMGS08682

SEQUENCE DESCRIPTION:

45 GATCTCTTGA ACTCTGGGTT CTCCAGCCC CTTGTCCTTC CTTCCAGETG AGCCCTGGCC 60
ACACTGGGGC TGCCTTTCTC TNACTCTGTC TTCCCAAGT AAGGGGGGCTC TCTNAGTGCA 120
GGGTCTGATG CTGAGTCCCA CTTAGCTTGG GGTGAGAACC AAGGGGGTTA ATAAATAACC 180
CTTGAAAAC GAAA 194

50 SEQ ID NO:7441

EP 0 679 716 A1

SEQUENCE LENGTH:132

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08683

SEQUENCE DESCRIPTION:

GATCANATGA AGAAAAGGAG AGGTAGATAC AGTCAGTGTC ACTTCAGGAA AGCTATTTAA 60

AAAANCTTGA AATATAATTG AAAGAAGAAA CAACACCAAA NAAGCCTAAN CCTAGCCTCT 120

GANCANCACT AN 132

SEQ ID NO:7442

SEQUENCE LENGTH:208

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08684

SEQUENCE DESCRIPTION:

GATCAATCTG AGGAGACTTA ATAATGATAT TNATTCTCCC AATTCATGAA TATAGTATAC 60

CCCTGTATTT ATTTGTNTTC TTGAATTCT TTTATCATTG TTTGTAGTT TTCACCATGA 120

CAGTCTTGCA CATATTTTGT TAAATGTACA GCTGAGAATT TAATTTTCC TGGTGACAA 180

TGCTAATAAA ATGGTGCTTT AAAAGAAA 208

SEQ ID NO:7443

SEQUENCE LENGTH:244

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08685

SEQUENCE DESCRIPTION:

GATCCTCTAA GGTCTACAG TTTACTTCTT GTATTCTCCT TTGTAAGTCA TCTCCAAGAC 60

GATGTCCAAA TCCATCACCA TTAATAATTA TAGTTTCCTC ACCCACAACA CTTAATATTT 120

TAAAAAANGA TACTTTTCAT TGTATTATAA TTAATTGATA CATACATATT TGCTCTGTGA 180

GTTCTTATT CATCATATTA GTGCCTGACA ATAAATGTGT GCTGGATTGA GCTGAATCTT 240

TAAA 244

SEQ ID NO:7444

SEQUENCE LENGTH:323

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08686

SEQUENCE DESCRIPTION:

GATCCTGCAA TTCCACTTAT AGGAATTGAC CCACAAGAAA TGAAAGCAGG GACTTGAACC 60

CATATTTGTA CACCAATATT CATAGCAGCT TATTCACAAG ACCCAAAAGG CAGAAGCAAC 120

CCAAATGTTT ATCAATGANT GATTGATTGG CTAAGCAAAA TGTGATATGT NCCTAACGAA 180

GTATCCTTCA GCCTGAAAGA GGAATGANGT ACTCATACAT GTTACAACAC GGACGAACCT 240

TGANANCTTT ATGCTAAGTG AAATAAGCCA GACATCANCA GATAANTAGT TTATGNTTCC 300

ACCTACATGN GGTACTGNNGA GTN 323

SEQ ID NO:7445

SEQUENCE LENGTH:318

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08687

SEQUENCE DESCRIPTION:

GATCCTCCTG CCTCATCCTC CCAAAATNCT GGGATTACAG GCATAAGCCA CCGTGCCTGG 60
 CCTCTTTAAT AATNTTNAAT ATACCCATAA GGCTTGTGAA TATACAAGTC TACTGATAAA 120
 TTATGTATTG TCTGGGAATT TGATAGTNAT TGTTTATAGT AACTGGNTTT TACGCTGTGG 180
 TAGNCNGGCT GTGACACTAG TGTTGCACAG GTGTAATTGG TCATCCTATG CCTTCACCAG 240
 AATAACTTGG GAGTGGTGCC AGAANCTAGA GTCTACAATT CTCACTGTTT AGAGAGTGTT 300
 ANTGNCATAC TGTGTATN 318

SEQ ID NO:7446

SEQUENCE LENGTH:317

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08688

SEQUENCE DESCRIPTION:

GATCAAGATA GTAGTATTAT TACACAAGAA ACTTGGTCTG CAGTCTGGAA GCTTGTCTGC 60
 TCTATAGAAA TGAAAATGCA GCATGAAGTT GACATTGTGG AAATGAAAGT AATTGGGTAT 120
 TAGAAATCTG AAAGTACTGT CATCTAANAG CAATTGTGAT TTTNTTGTA TGGTTGTCA 180
 CTGTTGTNCG GTGTCTAGNG TTANNGAATA CATGTNANCT TTCATGGTAT TTNGCCTTTC 240
 TTAANTTTTT TTAATAATTA ANCTTTCTAA CCTATGTATT CAACTTCTGT ATTTATATNT 300
 NATCAGTGGT TCATGTN 317

SEQ ID NO:7447

SEQUENCE LENGTH:284

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08689

SEQUENCE DESCRIPTION:

GATCATCAAA GAAAGACAGG GTGACCTGAG GATTATATGT TCAGCCAAGC TCCCCTCCAA 60
 GCATAAAGGC TACAGATAAC CATTGTACA TATTCAGGAA CTGGAGTAAT GTGATTCCAA 120
 TGAGCCTGTC TTGAAGGAAC TCCTAGGGGA TTAACCTCAG CTAACCTGGG AAGTTATCTG 180
 GAGAAACAC AACAGAAGGA CTGGTTGTAG TTCGAGGCTG TAGTCAGCTA TGATTGCACC 240
 ACTGCACTCT AGCCTGGATA ATAGAGCAAG ACTTTGTCTC CAAA 284

SEQ ID NO:7448

SEQUENCE LENGTH:324

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08690

SEQUENCE DESCRIPTION:

GATCCCTAGT ATAACACATT CAGTGTTCCT CTTTCAGTCT TACTACTTTN ACCGCGATGA 60

EP 0 679 716 A1

TGTGGCTTTN AAGAACTTTG CCAAATACTT TCTTCACCAA TCTCATGAGG AGAGGGAACA 120
 TGCTGAGAAA CTGATGAAGC TGCAGANCCA ACGAGGTGGC CGANTCTNCC TTCAGGATAT 180
 CAGGAAACCA GACTGTGATG ACTGGGAGAG CGGGCTGANT GCAATGGANG TGTGCATTAC 240
 ATTTGGAAAA AANTGTGAAT CAGTCACTAC TGGANCTGCA CAANCTNGCC ACTGNCAAAA 300
 TTGACCCCCN TTTGTNTGAC TTCN 324

SEQ ID NO:7449

SEQUENCE LENGTH:324

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08691

SEQUENCE DESCRIPTION:

GATCACCTGA GGTGAGGGGT TCGAGACCAG CCTGGCCAAC ACGGTGAANC CCATCTCTAC 60
 TAAAAATGCA AAAATTAGCC GGGCGTGGCG GCACATGCCT GTAATCCCAG CTACATGGGA 120
 GGCTGAGGTG GGAGAATTGC TTGAACCCAG GAGGCGGAGG CAGAGGCTNC AGTGACCCAA 180
 GATTGTGCCA CTGCACTCCA CCCTGGGCAA CAGAGCAAGA CCCCATCTCA AAAATAAATA 240
 ANTATATATA NAAATAAAAA NGCTATTTCT NGNNNNTTTC ACTATAAAGT TTTGCTTTAT 300
 TAAAAAGCTA NTANGCAGCT ATTN 324

SEQ ID NO:7450

SEQUENCE LENGTH:326

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08692

SEQUENCE DESCRIPTION:

GATCTTAAAC TCAGTAAGCC ACTATCTGCA ATTTTGTACA TTATATAGTA TTTTGAAGAT 60
 ATGGAACCTT ATGAAAAAAA AATAGCAAAT NAGTTCCTTT TCCCCCAGAG GGGAAAGTTA 120
 TGTNCTGCAA ATAGTGTGTG TCTTATTTA CTGTTGANCA GCAATNGCNN NTTATTTTTT 180
 NATTGCTTAG AACTTCAACA TGTGTATAG GAATCCTGTA GTGCCACTAG TTAATGCCG 240
 AATTCTCATC TGGATGTTAC CATCAAACAT CAGTACACTT GTCATTTCAC ATGTGTTTAA 300
 TGTGACAGTT TTTCAGTACT GTNTNN 326

SEQ ID NO:7451

SEQUENCE LENGTH:38

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08693

SEQUENCE DESCRIPTION:

GATCTNGTGG GCATAAATAA AGGTGTCATA AAGACAAA 38

SEQ ID NO:7452

SEQUENCE LENGTH:83

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08694

EP 0 679 716 A1

SEQUENCE DESCRIPTION:

GATCTTAAGA AGTGCTTTGA AGGGTTAAGA ATCAGGGGTC CAAGAGAGAC CCCAGTCCCT 60
CAATAAAGCC ACAAGAGCCC AAA 83

5

SEQ ID NO:7453

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

10

CLONE:HUMGS08695

SEQUENCE DESCRIPTION:

15

GATCTACACT CCAGGCCGGA AAGAGCAAGG GGAGCCCATG ACCCCTCGCC GCACGCCAGC 60
CCGCTTTGGT CTGTAAGCTG AGGCTGTCCC CAGAGAGGAT GGCAGCAGGT ATTGGGTCCT 120
CAGCCTTCTG GCGGGAGCCT GAGGCTGCGG ACAAAGCCCT TTAATCTAAG GACTTTAATC 180
TGTNCATATN ACGGCCCCC AGGGCAGTTC CTGCTGGACC AGACTCTNTG GCAGAGGAGG 240
TGGAGTTCTT CCATGCAGGA GCACGNCATG GCGGGAGCGG GGCTGCAGAG TATCCGNGGT 300
GCTGCCGNGG CACGGNGAGG TNGCTNGACC CATCGCATCT AAAANTAGGA N 351

20

SEQ ID NO:7454

SEQUENCE LENGTH:55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

25

CLONE:HUMGS08696

SEQUENCE DESCRIPTION:

GATCTAAGGT TTAAAAGAA TTTGGTTTGA AAATATACAG TTGTCTTGAA GGAAA 55

30

SEQ ID NO:7455

SEQUENCE LENGTH:61

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08697

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SEQUENCE DESCRIPTION:

GATCTGTTCT GTTTCACCAT GTAACACACA ATACATGCAT GCACTGTATT AGTGTTAGAA 60
A 61

40

SEQ ID NO:7456

SEQUENCE LENGTH:273

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08698

45

SEQUENCE DESCRIPTION:

50

GATCCCATTT TCCTCTGACG TCCACCTCCT ACCCCATAGG AGTTAGAAGT TAGGGTTTAG 60
GCATCATTTT GAGAATGCTG ACACTTTTTC AGGGCTGTGA TTGAGTGAGG GCATGGGTAA 120
AAATATTTCT TTAAGAAG GATGAACAAT TATATTTATA TTTCAGGTTA TATCCAATAG 180
TAGAGTTGGC TTTTNTTTT TTTTGGNCCA NGGGGGGGGG TTTTTCCTCC NTGCCCCCCT 240
GGGGTTTTTN NANTCCCNCT NNAAAAANAA ANN 273

55

SEQ ID NO:7457
SEQUENCE LENGTH:363
SEQUENCE TYPE:nucleic acid
5 TOPOLOGY:linear

CLONE:HUMGS08699

SEQUENCE DESCRIPTION:

GATCTTAACC AGTCGAGTGG AGTGTACATT GTCTGAATAC AGGNTGCACA ATGTTGTCAA 60
10 TCCTGGAAAT GGTCTTTCTT TTTTGTAAGA TATGTGAATG AAGTGTGGT GTCCTCACCA 120
AGAGGTGGCA CCTAAGGGTT CTGAGGAAAT AAATGTATAG ACCCTTATGT ACAGACCTGT 180
GTATAACAA CTNNTGTATA TACATATAGG ATAGCTTTT TGTACTATAC AGCTGGTACC 240
ATAANAGTAG CTGGATANTT TGGTTAGGNC NGGTTGTCCA CCAGTTTGG NNTTTTTTTT 300
CACTTTGNTN CATTTTGGGG GATTTTCCTT GTGGGTTGNN TAAAAANTG CATATGCTTA 360
15 NGN 363

SEQ ID NO:7458
SEQUENCE LENGTH:173
20 SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

CLONE:HUMGS08700

SEQUENCE DESCRIPTION:

GATCCGTATT TCCAATAAAA TCCCCTACCT GAATATTCAA GTTAAACATG TCCAGAATAC 60
25 TTAATGATTT TATTGTTAAT AGCCACTATT CTGTTGTCTG GAATTAAAAC CTGTATAACT 120
AATTTGCATC CCTTTATCTT CTTAGTCAAT AAAACCTACA ATCCTCTTTC AAA 173

SEQ ID NO:7459
30 SEQUENCE LENGTH:349
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08701

SEQUENCE DESCRIPTION:

GATCACCCCC CAACTTGCCC TTCAAGTTCT ACTTCAGTTT GATAAGGCTA TAAATGCAGC 60
35 ACTGGCTCAG AGGGTCAGGA ACAGAGTCAA TTTCAGGGGC TCTCTAAATA CGTACAGATT 120
CTGCGATAAT GTGTGGACTT TTGTACTGAA TGATGTTGAA TTCAGAGAGG TGACAGAACT 180
TATTAAAGTG GATAAAGTGA AAATTGTAGC CTGTGATGGT AAAAATACTG GCTCCAATAC 240
40 TACAGANTGG ATAGAAAANN TATGACTNNT TTACACCATC TTCCTGTTAT TCATTGCTTT 300
TTGAAGAGNA GCATAGANGA GACTTTNTTN TTTTATNCTN GGAATTTN 349

SEQ ID NO:7460
45 SEQUENCE LENGTH:395
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08702

SEQUENCE DESCRIPTION:

GATCTGGAGT AAGGAATATT GTCATCACCT GGATTTTGAG AAAGAAAAAT AACTTCTCTG 60
50

EP 0 679 716 A1

CAAGATTTCA TAATTGAGAG AATTCCTGAG TTGATAGCTC TAAAGGCAGA TATGCTGTAT 120
 TTGCCTACTT TAACCCATTI TTCAACCTGT TTGTTTTTTA ANNGGNTTCA CTAAGGGTTG 180
 ATATGTACCA TTGTATGGGG CAATTTTAAG TCAGCTAAGG CAATAACCTT ATGCATGAGC 240
 ATTTCCCGAGA CTTTCATGAA GCTGTTGAGG TCCTAGGCAA TTAATGCAGC AGTTGCGATA 300
 AATAAANGNC NTCTCACCTA AGNNTCCNTT TTCTTCNATA ACCATGGTTC CTGGNCATGN 360
 TTGGGAGGCT NCTCGGCTTT AGGGNAANGG GGTTN 395

SEQ ID NO:7461

SEQUENCE LENGTH:347

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08703

SEQUENCE DESCRIPTION:

GATCGCCTCC CAACAGCAGA TTTGACATT ACCTGAGAGT CTTGATTTTA GGCTTGTTTT 60
 TTGTAAACCC ATGTGTTTGT AGAGATTTTA GCGCTCTTCG GATATCTTCT CACCTATGTT 120
 CCCTGGCTAA GAAGTCAGAG GTAGCCAATG TTTCCTTAAA TTCATTTTAA AACTTACCAT 180
 TGGTGCCATAT GTTCCAGATG GCAGATGCTG TCAATAATCT CACCATTGAT GACCTTTGTG 240
 TATGTAGTTC TTGCATCCTA TACTGGATAA GCCTGTTTTA ACCTGCTATG ATGGGTGCTT 300
 TCCATTGCTT CNTAATCTTC ATGGAGGGTT GCCATGCTTT TTGCCNN 347

SEQ ID NO:7462

SEQUENCE LENGTH:274

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08704

SEQUENCE DESCRIPTION:

GATCGGNATG TAATAACAGC ATTAATCAC AGACCTTGGA GCCTAAGCCA TACAGGAGAT 60
 GGGAAACCAC GCTATGATAC TTNCTGGAAA CATTITATAT TTNTAATGAT GGACATTTN 120
 CTCGATTGGA GCATGCATAA TANCITGTGG TACCTGTGTG GAATTTTANC TTTCTCATG 180
 CAAAAGGATT TTNATCCCC GGCCTACTTG ANGAAGTGGT CAGCTAANGG NNTCCAGGTT 240
 GTTGGTTGGA CTGTAATACC NTTTGATGAN AAGN 274

SEQ ID NO:7463

SEQUENCE LENGTH:69

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08705

SEQUENCE DESCRIPTION:

GATCAGAAAC TTGCATATGC GTGAAAAAAG GAAGAGCAGC AGAAAAATAA TAAATGACAG 60
 GAAAGCAAA 69

SEQ ID NO:7464

SEQUENCE LENGTH:199

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

EP 0 679 716 A1

CLONE:HUMGS08706

SEQUENCE DESCRIPTION:

5 GATCTATAGC AATGTGATTT TATTTTAAA AAGAAAAGCA GTGTGTTTC TTTTTTGTT 60
 GTTTTCTTT GCTTAAGCAC TTCATCAATT GCTTTATTCT GTATCTGCGA AGTNATCTGC 120
 AATCTCNTT GNNCTTTNTA AAATTTGGAT NTGTTATAAA AATTGNCCAN ATTGGAAGGT 180
 GTTTCAGTTA AAAAAANAN 199

SEQ ID NO:7465

10 SEQUENCE LENGTH:320

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08707

15 SEQUENCE DESCRIPTION:

GATCACAAAC TTGGAGGGCT GTATGGTTTT TCATTTAAGA AAGTAATTGT CGTGCAATAA 60
 AGTTATTAAG CCTTGTTTAA GAATATTTT ATTTGTACA TCAAGTGGAG TTGGAAATAG 120
 TTGGTTTCAT AATGATATAT TTCAAAAGTA TCTGAAGTC ATCTGGTTCA TTCACTACC 180
 CAGGGCACAC ATTCCTCCTG TAACATCCCA AGTGTTTATT AAGCAAAACA GATTATTTT 240
 20 ATTTAGAAAA NNTTAGTATG ACTGATTGC TATTGATTT GTACTTCTAT AAATNAATGT 300
 GGATACATGC TATATTCAA 320

SEQ ID NO:7466

25 SEQUENCE LENGTH:311

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08708

SEQUENCE DESCRIPTION:

30 GATCACTTAC AGGTGCCCTC TCCCCAACA GCCAGAAAGG GAAAACAGAG CCGAGTTTGG 60
 CCACTGGGGC CTCCACAGCC CTCTGGAAGA AGGGGCTGAC TGATAGGAAG GCACTCCTCT 120
 GGTGTTCACT GGCCAGACCC CTGTGGGCTC AGAAGACTAC CTAGACCCCA TGAAGAAAGA 180
 CTCTAGACAC ATTTTATAA TCAGAACTT ACAGTTTATT GTGAATAAAC CACTCAACTT 240
 35 TGAGCAGATG ACATTGCCTC ANTTAACTTT TTCGTTGAAG AAAACAAAG ATATATGGTA 300
 AATTCATGAA A 311

SEQ ID NO:7467

40 SEQUENCE LENGTH:434

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08709

SEQUENCE DESCRIPTION:

45 GATCATCAAC AAAGACTTGT TAGAAAGGTC TAGTCTTAGC ACTTGGCAGT TAATCTAGGG 60
 AAGATGAATT AAATGGGTAG ATAGTGATGC ATACCTGTAT TCACTGATGT ATGTTTAAGG 120
 GATTTGGGGG GGATACCTCA GTTCATGTGG AAGGGACAGT CTCGGTGTGT CCCATGAATA 180
 ACCTTGGAAC TGCAACAAAT GGTTTGTGCT CAGAAAAAGT CTTTCATGGT GACAGGAAGA 240
 CAGTTTCCCT GGAGCTGGCC ATGAAGGCCT TAGAAGCCAT TTCTGGTGTC TGGTGGGTAG 300
 50 CAGGCATAGA GATGATGTNC CGAGGTCCCA GTGAACACCA GTAGCCAAAN GAATTGTACT 360

55

ACCTTNTATC CATTANTTNG GGGGAAGGTCC TTCCTNNGG NAACCAATGN CCTTTTTTGN 420
TGGGCCAAAA TTTN 434

5 SEQ ID NO:7468
SEQUENCE LENGTH:414
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
10 CLONE:HUMGS08710
SEQUENCE DESCRIPTION:
GATCGAGCTG TGGACTTATA CCTGTGTGCN TGGTTTACAG GTCCAGTGGT TCTTCAGCCC 60
ATGACAGATG AGAAGGGGCT ATATTGAAGG GCAAAGAGGA ACTGTTGTTT GAATTTTCCT 120
GAGAGCCTGG CTTAGTGCTG GGCCTTCTCT TAAACCTCAT TACAATNAGG TTAGTACTTT 180
15 TAGTCCTGT TTTACAGGGG TTAGAATAGA CTGTTAAGGG GCAACTGAGA AAGAACAGAG 240
AAGTGACAGC TAGGGGTTGA GAGGGGCCAG AAAAACATGA NTGCAGGCAG ATTCGTGAA 300
ATCTGCCACC ACTTTATANC CAGATGGTTC CTTTACAAC CCTGGGTCAA AAAGAGAATA 360
NTTGGCCTA TNATGTTANA AGGAANGCAG GNNGGTGGGT TNAANTAAAA NTTN 414

20 SEQ ID NO:7469
SEQUENCE LENGTH:214
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
25 CLONE:HUMGS08711
SEQUENCE DESCRIPTION:
GATCAGTATT TTTAATCAAC ACCTGAGAAC TGTTACACCT TTNATTTTGT CTTNAGGAA 60
ATCCCTGTCT TTCCATTTT TCATGTAAAT NTTGCACAGT TACTTGTTCA TATGTAAATA 120
TTTTACTTTC AGAAATNAAG TTTTAAATTG CTATTGTTTT ATATAGGATT GAAAGAAAAT 180
30 NAACTCCTTT ATTAATAACA AATTTATCTG TAAA 214

SEQ ID NO:7470
SEQUENCE LENGTH:418
35 SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08712
SEQUENCE DESCRIPTION:
40 GATCCATTTT CTCAGGACTC AGTTAGGTGT GCCCAGACGC ACTGACAAAA TNACGTGACT 60
TCAGGGAAGC CTGGACACCC GAGGCACCTG GACCAGCTAT GGGTAGTTCT GTGGGTGGAA 120
CACATTCTGT GTAAGAGCCC CACTGAGGGC TCTGCAGCGG AGTGACAGCA ACCCCAGAGA 180
TGAGGCACCA GAGAGTGCCA CTGCATGAGA CACCTGTGAC CATTGAAAGT CTGAAATGCG 240
GGGGGGGAGT TTCATTTTTA AGTGAAGACC AAAAGCCCTT TAAAAATAAT AGTTTTTTAT 300
45 CATTTTATAG TAATCAGCGG NNTCTCTTTT ACTAATATAC TCATTCTNT TCGGTATGAT 360
TGGNCTTTTG GAGCTACATG CTCNACAAN NCTGTATCTT AATTGGTTAA CTTGTTAN 418

50 SEQ ID NO:7471
SEQUENCE LENGTH:422
SEQUENCE TYPE:nucleic acid

55

TOPOLOGY:linear

CLONE:HUMGS08713

SEQUENCE DESCRIPTION:

5 GATCTTGCGG TTGTGGTAGA TTGCCTTCCT GTGCTCACCA ATTGTTTACA GGAAGAAAAA 60
 CAATATATCT CACTTGGCTG CTGTGTTGAC TTGTTGCCTC TAGTAAAGTC ACTACTTAAA 120
 AGCAAAATTN AAGAATATGT TATAGTTGGT TTAAACTGGC TTCAAGCAGT CATTAAAAGG 180
 TGGTGGTCAG AACTATCATC CAAAACAGGA ATTATAAATG ATGGAAATAT TCAAATTTTA 240
 10 AAACAACAAT TAAGTGGATT ATGGGTACAG GANAACCATC TTAAGTTGGT TCCAGGATAT 300
 ACTGGTAATN TAGCTANGGG TGTAGNTGCT TTTTTCTTT CCAGTTCNT TGNGGGATT 360
 CCTCTNCCTG NGGGGCATTT TGGTTTTCA ANACNTCCC NTGGACCTGT TTTANTTTTC 420
 CN 422

15 SEQ ID NO:7472

SEQUENCE LENGTH:359

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08714

20 SEQUENCE DESCRIPTION:

GATCGCCTTA ACTACTGTAA ACATAGCCTA TTTTGTGCT TAANATACTG AATGGAAAAC 60
 TCCATTGTGT GTTGTGGAC TGTTTGGAA ATATNNNGTT AAATGTGTGT TAATTGGCT 120
 GTAATGGCAT TTAAAGCAA CAAACAAACA AAAAAAGCTG TGAAAATGGC CTTGGAGCAT 180
 25 TATCTTTAGT TACTTGAAGA GTTCTAGTT TTTTAAAT ACAGTTTATG TTAAATAAT 240
 TTTANTTAAT TTAGAGANGC CAATCATTGT CTGNGGGGAA ACCGGCCTN CNNTTTGGGN 300
 TTNCTTTTN GTGGGCCATT GGTGAGGTGA GTGCCTNTN CCCGTTTCNT TNGGTTTCN 359

30 SEQ ID NO:7473

SEQUENCE LENGTH:105

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08715

35 SEQUENCE DESCRIPTION:

GATCTTTAAA GTTATTTTAA GGCACATTG TGACAAACAA CTAAGTATA TTGAAATCTC 60
 CNTAGCCAT TAGAAGCTAT CAAATAAAGT AGGTGTAATA ACAA 105

40 SEQ ID NO:7474

SEQUENCE LENGTH:104

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08716

45 SEQUENCE DESCRIPTION:

GATCAAGTAT GCTAATNTTA AGCAAATGTA AAACTCATA AAACAGGTAA ACAGTGGGGT 60
 GATTTCATTT GCCATAATTC ACATAAGACG AATTTTAATC TAAA 104

50 SEQ ID NO:7475

SEQUENCE LENGTH:340

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08717

SEQUENCE DESCRIPTION:

GATCCTTGTT TTAAAGTTAC TTTCGATGTG TATACGAACA AAGACCAGGG AGAAACAGAA 60
 CTTTTAAAC TATAGGCTGC TGTNTTGGGG CCAGAAATAA GGTGACAAGT AAAGACTTTT 120
 ATAATACCTA CCTTCAAANT TAGAATCAGC AGCACTGTAC AANTAAAGTG CCTGTGCTTC 180
 ACCTCACACC AAGANTCTTG CCTAACCTG TCAGAGTGCC TAATATCCTG TGGTGATTAT 240
 GTATAATGAA ACAGTCTTAT TTTGTGCTCT TTGGTTTCTT AAAAGGAAAG CTGTTTCT 300
 TTCCTTTATC ATTACAGAGG TATGTCTTG GTTCTTANTN 340

SEQ ID NO:7476

SEQUENCE LENGTH:189

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08718

SEQUENCE DESCRIPTION:

GATCTGTGAA AAAATACAGT ATTGTAAATC CAAGACTCTG ATACTGAATT TAAGTTATTT 60
 CACAGTTGTA GCTACACAGT AAGTAGCTTG GTAGATAGTT ATTGANTGTA TTTATGTAGT 120
 GTATTAAGAA GCTTATATTA CTACAAAAA CTTATTTTAA TATATNTNNN TATNTNNGTN 180
 TTATTTATN 189

SEQ ID NO:7477

SEQUENCE LENGTH:342

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08719

SEQUENCE DESCRIPTION:

GATCTGTGTG AAAAAATNAT TTCTTAGCTA TAATCAGCAC ATCACTTAGT TCAAACAAAA 60
 TTCCCAGCA AATGTTAGAT AGTAGGTATA TCAGTCACCT GGGGAGTTTT CTCATAATA 120
 TGCATATTCA TCTNGTAATG CATACATAGT TATCATCCTC CTTCTCAACC CATCTCCCTA 180
 ACCCCACATG CTGCCAGTT CTTGAAGGGA TAAAGTGATT GTAATAGTGT TTNACTNCTC 240
 TCTGTTCAAT TTANTGTGAT ATAATTCTAG TTAANNNTA TTTNGGACAG TNGCTTAACC 300
 ATGGTCATAA GAGGATTGT ACTATAGATT ATCTTCNGGG GN 342

SEQ ID NO:7478

SEQUENCE LENGTH:54

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08720

SEQUENCE DESCRIPTION:

GATCTTTGTC AACCAAAACA TGTATTTTCA ATAAATTGAG ATTCCCAGTT CAAA 54

SEQ ID NO:7479

SEQUENCE LENGTH:79

EP 0 679 716 A1

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08721

SEQUENCE DESCRIPTION:

GATCTGTTTC CCTTTCACAT TTTCCCCATT TTGTGAGCAT TTCCTTACTT CCTAACATGA 60
CAAAATATTT CAAACTAAA 79

SEQ ID NO:7480

SEQUENCE LENGTH:281

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08722

SEQUENCE DESCRIPTION:

GATCCCCCTG GCCTGGAGGC AGCAGCTGTA TAAACTCTAC GAGGCCGACT TTGTTCTCTT 60
CGGCTACCCC AAGCCCGAAA ACCTCCTCCG AGACTGAAAG CTTTCGCGTT GCTTTTCTC 120
GCGTGCCTGG AACCTGACGC ACGGCACTC CAGTTTTTTT ATGACCTACG ATTTTGCAAT 180
CTGGGCTTCT TGTTCACCTC ACTGCCTCTA TCCATTGAGT ACTGTATCGA TATTGTTTTT 240
TAAGATTAAT ATATTCAGG TATTTAATAC GAAATGTGAA A 281

SEQ ID NO:7481

SEQUENCE LENGTH:326

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08723

SEQUENCE DESCRIPTION:

GATCTGAGTC CAGGCAGTGT TTTTAAGNGA TATGAGTTAG TAGTGAAAAT TGAAAAGGAT 60
ATTTTACAAC CAAATACAGG TTTNNTGGTG TTTTTGAAA AATCCAAAGA TTTGGCAACT 120
CGACCTAGGC TCCGACAAAA CCACAGTTGT TGGGAGCTGA GCCGGAGCCA GAACTCACAA 180
TTCACCGTGG CCCGGCCACC CATCCCCACC ACTCCCGTGG GCTCCTGACC AAGCACCACG 240
TGCCATTCAT CATGGCTTGC TTTTAGTGTT TTTGGTGTTT ATCTTAAAGT ACAGCGAAGA 300
AGAAAGGGAA GTATTTNTTA GACCCN 326

SEQ ID NO:7482

SEQUENCE LENGTH:331

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08724

SEQUENCE DESCRIPTION:

GATCTGGATT TGGTAAAGGT TGACTTAATT GAACTCTCTG AAAAATGCTG TAGTGACTTT 60
AATTTGCACT CAGAATTAGA GCGCTCATTT TTGTCAGANC CATCATCTCC AGGAAGAACC 120
AAGACTACTA AAGGATTCAA ACTTGGGAAG CACAAGCATG AGACCTTTAT AACGTCAAGT 180
GGAAAATCTG ANTACATTGA NCCTGCCAAA AGAGCTCATG TTGTGCCACC ACCAAGAGGA 240
AGGGGCAGGG GTGGNTTTGG ACAGGTATA CGACCTCATG ATATTTTNG TCAGNGNAAC 300
CAGNNCACAN GTNGACCACC ATCTNTGCNT N 331

SEQ ID NO:7483

SEQUENCE LENGTH:338

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08725

SEQUENCE DESCRIPTION:

GATCGGAGTC GCCAGGCAGT ATATCCAGTT AGAACTTCCG GGCTTTTGCA TTAGCTTGTC 60
TGATGCTCAT GCCCCACTCA GAGAAAAGAC ATCAGCAAAT TAAGAATTTT CTGGGTTCCCT 120
GTGACCCTCA GGTtATTTTA AAGCAATTGG AAGAGCATAT GAACACGGGC CAGCTAGCAG 180
GATTTTCACA TCAAATTAGA AGTCTGATTT TGANTAATAT CATCAATAAG AAGGAGTTTG 240
GGATTTTGGC AAAGACCAAA TACTTTCAAA TGTGAAGAT GCATGCGATG AATACCAACA 300
ATATCACTGA GCTAGTGAAC TATTTGGCAA ATGACTTN 338

SEQ ID NO:7484

SEQUENCE LENGTH:338

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08726

SEQUENCE DESCRIPTION:

GATCCGCCCT CCTTAGCCTC CCAATCCTCT CTTAAAAAAG TGATAGCTCA GAAATATTTG 60
TAAAAGCAAG GTTTTATTTT CATTTTGGCT CTGTCATTTT CAGAGGCAAA GAAGTTGGCC 120
TGTAAGTAG AGTGCTAGAG CTCTTACGCC CCTCCCCTTC TTCCCAACTT CCTACTTCCT 180
AGCCCTTTTA TCAACTCCTA GAATAGTTAA AGAGAGACAC ATCTAGATGG GATGAAAGGT 240
GCCCTAAGCA GGAGAACCTG ANCAAAAGGC TAGAGGCATG GGCCAGGTAA AATTGGGGC 300
CTAGAGTGAA GNCTGTGCTG TCGTTAAGNG CTTTCGAN 338

SEQ ID NO:7485

SEQUENCE LENGTH:338

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08727

SEQUENCE DESCRIPTION:

GATCACAGTG ACAAAGAAGA TGAACAGCCT CAAGTGGTGG TTTTAAAAA GGGAGACCTG 60
TCAGTTGAAG AAGTCATGAA AATTAAAGCA GAAATAAAGG CTGCCAAAGC AGATGAAGAA 120
CCAACCTCCAG CCGATGGAAG ANTCATATAT CGAAAACCAG TCAAGCATCC CTCAGATGAA 180
AANTATTCAG GTTTAACAGC AAGCTCAAAA AAGAAGAAGC CAAATGAAGA TGAAGTAAAT 240
CAGGACTCGG TCAAAAAGAN CTCACAAAAN CAANTTAANA TTAGTAGCCT CCTTCTTTT 300
GACAACGAGG ATGAAAATGA GTAAGTGTA TTTTTTN 338

SEQ ID NO:7486

SEQUENCE LENGTH:302

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08728

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCTTAATT CATATCTTGA AGATAAAGTC TACCTTACAG GGTATAACTT TACATTAGCA 60
 GATATACTAT TGTACTATGG ACTTCATCGC TTTATAGTGA GTATTTGTAT AGTTACTGGC 120
 TTTTCTCTG TAGTGTGAG AATGATTTT AAAACTTTGT CTTGAATTTA AATCAGATTT 180
 GCATTTTGG CTTATCAAAAT AAAAATGAAA GGAATTCCTT TATACAAGGT GCCTTTTGTA 240
 ACAAACCTGC ACGTTGTGAC ATGTACCCTA AACTTAAAG TATAATANTA ATAANNTTNA 300
 AA 302

SEQ ID NO:7487

SEQUENCE LENGTH:334

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08729

SEQUENCE DESCRIPTION:

GATCAAAAGT GAATAATGTA TGAATGAGAG CTGTAAGAAG GATTTTNATT TTGTTATAAT 60
 TTAGTTACCA TTTTCAGTGT TATTTCAAAG GTTCTTTGAA GAATTTTGGG GCAGGGCATC 120
 AGATTAGAGT TTTAAAAATT GAGTATTTTG GATATCAGTG TTCCTCATGA AGATATACAT 180
 GGATATNCAA TTTTGATGGC TTCCAGATTT GTAAGATTTT ATGTTGTATA TACCATTCTA 240
 TTAAGAAACA TGTCCACTGT GCTTTCAAAC ATAGATAAAG CATGATAAAG ATTATNATT 300
 AAGATATACT TGTATTTATA CCTCAGATAT TCTN 334

SEQ ID NO:7488

SEQUENCE LENGTH:337

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08730

SEQUENCE DESCRIPTION:

GATCAGCTGG ATACTCNTGT NACCAGAATT CCAAAGGTTT TGATAGAATC AAAGATGGAT 60
 ACAAAGTGAA CTCACACATA GCTAAGCTGC AAGAGTTATG GAAAACTCCC CAAAATCAAA 120
 CAATCCACCT CTCTAANTCA NTGATGGAGG CGTCCTTTT CAAGCATCCA GACCTCACCA 180
 CAGGCCAGAN GCGTTACCNG TGCAGCATTG CTAAANTCTA TAATGCAAAC TATCTGANGA 240
 TGTTAATGNA GNGGCAGTAC ATGCACGTNC TTCAGCACAG CTCACAAAAG CCAGGTGTCC 300
 TCACTCATCA CAGNNGCCGC CTTNGCTCCC GTTTATN 337

SEQ ID NO:7489

SEQUENCE LENGTH:292

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08731

SEQUENCE DESCRIPTION:

GATCATTGAG AACACTGNAC ACAGCAGCTT CAGGCAAAGG GAAAAGAACT AAATGAATTC 60
 CGGGAAAAGC ACAACATTCG TCTCATGGGA GAAGATGAGA AGCCAGCAGC CAAGGAAAAC 120
 TCAGAAAGGG CTGGGGCTAA GGCCAGCTCA GCTGGAGTGT TGGTCTCCTA GGGACCAAGG 180
 CCTTTGCATT TTTTCTACC CTGACTCCCA CTTCTAATTT CTCTTTATTG TTATTATTAT 240
 TATTTTCTCT GCTATTGTAA TATTTTTTGT TTAATTAAAT GTTTTGGTTA AA 292

EP 0 679 716 A1

SEQ ID NO:7490

SEQUENCE LENGTH:140

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08732

SEQUENCE DESCRIPTION:

GATCAACTGC AAACAGGCAC GAAGGAACTT TTTTGGGTGA TGA AAAATAA AACTTTGGAT 60
 GTCGAACATA TTTTGAAACT AGATTGCAAT NATAGTTGCA TAACTNTATA CATTATTAA 120
 AATCGTGGAA CACTTACAAA 140

SEQ ID NO:7491

SEQUENCE LENGTH:337

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08733

SEQUENCE DESCRIPTION:

GATCCGGTCT CCCCCCCCC CCGGCTGCAG GGTGGATAAA GAGGAAGATG TGAAGAGGAG 60
 GCAGACAAAA GCAAAAGGAC ATCCTGTCAG TAGGAAACGG CCGAATTACA ATTCAGATGT 120
 GCAATGTTTG CATAAGTAAA CTGACACGGG ACTATTATAT GCAGAANTCC ACGTGCAAAA 180
 NTTTTCAGAC ACACCTTTGT ACCTCTNCCT AATCCTGCCC TGGTAAATG GCGGTTATCA 240
 GTGCAAGTTT GAGGATACAT ACAGCTGGAA ANTGGNCATC ACCAACTGG ACTCCAGAAA 300
 GTNCTGTCTA GGATTTTATT AGACTGCTTT TTTNCAN 337

SEQ ID NO:7492

SEQUENCE LENGTH:337

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08734

SEQUENCE DESCRIPTION:

GATCTATTTT TCAGTAATNA GTGTGTGCCT CATGCCTGTT TCAATATTGG GTTTGGAGA 60
 CANTATTGTA CCAGGCCTGT TGATTGCATA CTGTAGAAGA TTTGATGTTT AGACTGGTTC 120
 TCCTTACATA TACTATGTTT CGTCTACAGT TGCCTATGCT ATTGGCATGA TACTTACATT 180
 TNTNGTCCTG GTGCTGATGA AAAAGGGGCA ACCTGCTCTC CTCTATTTAG TACCTTGCAC 240
 ACTTATTACT GCCTCANTTG TTGCCTGGAG ACGTAAGGAA ATGNAAAAGT TCTGAAAGG 300
 TAACAGCTAT CAGATGATGG ACCATTGGN TTGTCAN 337

SEQ ID NO:7493

SEQUENCE LENGTH:75

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08735

SEQUENCE DESCRIPTION:

GATCGGCCTG CGAAAGGATA CTGTGAAATN ACTAATTAAC TAATAAACCT GTCTCAAGTT 60
 GAGGATTTGA AGAAA 75

SEQ ID NO:7494

SEQUENCE LENGTH:343

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08736

SEQUENCE DESCRIPTION:

GATCTGGGGT ACTTGGCAGG GCTTCCCTCA GACAATACCT TAGAGAGTCA CAACCATTCC 60
 AGGGTCTGGT CTACCTCACA TCCTCATTCA TTGTTGGATG TGCTTAGCAT AGCCAGAGGT 120
 GTCTTCTCTT TGACAGACTT GCTATCTGAA AAATAAACCA GGACACCAAT TTTTATAGCAT 180
 ATAATAGAGG ACATCCCTTC CCAGCTATAG GAATGCTTGG TATCCTTCCA AGAACTCCTC 240
 CTTTAGAGGA GCCTCACAGA AGTTGCTGGG TAAACATGGG CTCAAACCAA GGAAAGTCAG 300
 GTAACCTGGG TGGNGGTTAT CCCACCACCA ATGGCAGGGG GTN 343

SEQ ID NO:7495

SEQUENCE LENGTH:95

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08737

SEQUENCE DESCRIPTION:

GATCAATATT GTAAAGAATT TATTCTGATA AATNAGAAAC TGGATATAAT GTCAAAATAG 60
 CTATTTTCTC AATAAAAAATC TCAAATCTCC TGAAA 95

SEQ ID NO:7496

SEQUENCE LENGTH:143

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08738

SEQUENCE DESCRIPTION:

GATCCTCCCT CCTTGGCCCC CCAGTGTTGG GATTACAGGC ATGAGCCACC GTGCTTGGCC 60
 TGGAATNAAT TTTTATTGTA AGTTATTCTG TATCTCCAGT GTTGGCATAT GCTAGACATT 120
 CAATGAATAT TTGTTGATTT AAA 143

SEQ ID NO:7497

SEQUENCE LENGTH:342

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08739

SEQUENCE DESCRIPTION:

GATCAACAAA ATGTGGTATA TTCATACAGT GGAATATTAT TCAGCCTCTA AAAGGAAGAT 60
 ACGCTGACAT GTGCTGCAAC ATGGATGANT CTTGAGGACA TGATGCTAAG TGAAGTAAGC 120
 CAGTCACTGG AAGACAAATA CTCTATGCTT CCNTTATGT GAAGTATCTA GAGCAGTCAA 180
 ATGCATAGAA ACAAGTAGAA TGGTAGTTGC CAAGGACTGG GGGAGGAGGA AATGAGGAGT 240
 TGTTTAATGG GTATAGTGTT TCATTTTTCG NAGATAAAAA GTCCTGTGGN TTGGTTGCAC 300
 AGTTAAGTTA TGTGANTGCT GTATGCCCAA CTCANCTGTT NN 342

EP 0 679 716 A1

SEQ ID NO:7498

SEQUENCE LENGTH:236

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08740

SEQUENCE DESCRIPTION:

GATCCAGTCG GCCTGGAGAT TCTACGCCAC CAACCTCTCG CGCACAGACC TGCCTCCAC 60

GTGGCAGTAC TACGAGCGAA CGGTCACCGT GCCCATGTAC AGGTACCGCC GCCGGGCACC 120

TGCCACCAAG CAACTGTTTC ATTTTATT TTCCATTGT TCTTAAACCC CACTTTTGT 180

TGTTCAATTAT TTTGATTGAT TTTNNNTTCT TTAAATGTA TTTTTCACAA AGGAAA 236

SEQ ID NO:7499

SEQUENCE LENGTH:160

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08741

SEQUENCE DESCRIPTION:

GATCCTAACC CTTTAGTATG CTGGAATTCT ACTCTTCACT TACTGCATTG ACTGTTGTTG 60

ATTAGTTATN ATTGCAAAGC ACTGTCACCG GCCTCAGGGA GTTTATGTGT AATAGAATTA 120

AAAATAATAG CTGTGTATAA CACTTAGCTC AAGCCACAAA 160

SEQ ID NO:7500

SEQUENCE LENGTH:210

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08742

SEQUENCE DESCRIPTION:

GATCTTATTG TGGAGTTAAA CAAAGCACCC TTAAAGTAGC AAGCGAGCAA AATAAAAGCA 60

AGGAAAATCA GTTGAACAT AACTTATGTA TTTTITAGGA TTAAGAGTAA TTTAACTGAG 120

TCAATTCAAT ATGTTTTTAA AGGTGTGATT CTAAATNCT TTATGATTGT TTAGATTCT 180

ATATCTTGGT AACATGAATA CACTTAAA 210

SEQ ID NO:7501

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08743

SEQUENCE DESCRIPTION:

GATCAGCATT TGTATTNAG TCCATTAATG GGAAAAATAG CTGATATTGT NCATAGGAAC 60

TTGGAAACCA CACAGGACTT AAGTCCCTTG TCTGTNTGA TGGTCAACAT ATCTCCTTTA 120

ATATCAGGAC ATTTTCAACA ACANCTGGTG AACAAAACAG ANCTNCTTTT TGACACCATA 180

GATTCTCCTG AGGTCAACGT TGCAAAANGC ATAGCAAAGT TNCTCCGAAA TGTTAGATAT 240

CGTTATCAAC CACTATTAGA CAGATGTAAT ACCGTATTTT TTCAGTAATG TGGNCCACCT 300

TGATTTTGGN TTCCATCAGT ANAGNAGCTT AGTGATACA NNNACNAAAN N 351

EP 0 679 716 A1

SEQ ID NO:7502
SEQUENCE LENGTH:195
SEQUENCE TYPE:nucleic acid
5 TOPOLOGY:linear
CLONE:HUMGS08744
SEQUENCE DESCRIPTION:
GATCGCACCA CTNCACTCCA GCCTAGGTGA CAGAGGGGAT GACAGAGGGT GCTCTGCGNN 60
CAGGGAAGGC GGGGTGGTTG GGGGGTAGAG AATGTTGCNC TNATAACCAC AGCTGTGGTT 120
10 ATTTTNTGGC AGGTACAGGT NAGGTTCCCT CTCCTTTCCA CCAGATGGCA CTGGAGAAAA 180
GGGATTTNAN TTAAN 195

SEQ ID NO:7503
15 SEQUENCE LENGTH:257
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08745
SEQUENCE DESCRIPTION:
20 GATCAGAGCA GAAATAAGTG AAATAGAGAC TAAAAAATAG AAAACATCAA TGAAACAAAG 60
AATTATTTTT TAAAAAGATA AACTAAATTG ACAAACCTTT AGCTAGACAA AGAAAAAAGA 120
GATAAGACAC AGATAANTAA NTTCAGAGAT TAANAAGAAG CCATTATACC TGATACCACA 180
GAANTACAGA GANTCATAAG AGACANTTAT GTTGTGCACA TGTACCCTAG ANCTTAAAGT 240
25 ATAATANNCN NTANTTN 257

SEQ ID NO:7504
SEQUENCE LENGTH:328
SEQUENCE TYPE:nucleic acid
30 TOPOLOGY:linear
CLONE:HUMGS08746
SEQUENCE DESCRIPTION:
GATCTTACAG AGAAAGACTA TGAAATACTT TTCAAATCTA TTAATGGAAT CCTTTNCCCT 60
35 GGAGGGAAGTG TTGACCTCAN ACGCTCAGAT TATGCTAAAG TGGCCAAAAT ATTTNATAAC 120
TTGTCCATAC AGAGTTTGA TGATGGAGAC TATTNCCCTG TGTGGGGCAC ATGCCTTGGA 180
TTTGAAGAGC TTTCAGTCT GATTAGTGGA GAGTGCTTAT NAATTGCCAC AGATACTGTT 240
GACGTGGCAA TGCCGCTGAN CTTCACTGGA GGTCAANTTC ACAGCAGAAT GTNCCAGANT 300
40 TTCCCTACTG AGTTGTTGCT GTCATTAN 328

SEQ ID NO:7505
SEQUENCE LENGTH:102
SEQUENCE TYPE:nucleic acid
45 TOPOLOGY:linear
CLONE:HUMGS08747
SEQUENCE DESCRIPTION:
GATCAATTG AAGTCCCTGT TTGGGAATAA GGCACCTATC AGCATGAAGA ATTTTTTCTC 60
50 ATTCTGTGCC ATTTTAAAA TAGAATACAT TTGTATATTA AA 102

EP 0 679 716 A1

SEQ ID NO:7506

SEQUENCE LENGTH:343

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08748

SEQUENCE DESCRIPTION:

GATCACCTTC GNACGACTAC ATCGCCTGCT GCGTCAAACCT GAGGGCTCTT ACAGNCAGTT 60
TTCGAAGNCG GGGTACTGCT CAGCAAGGTG TTGTGAATTT CCCATATGAT GATTTCATTC 120
AATGTGTCAT GAGTGTITTA ATCAAGAGGA AGCTGCATGA ATGTAATCAA CATTCCAACT 180
GGAGCTCTCC TTGCTTGTG CTCTTTGCCT TCGGTAATAT GTATAAACTT ACATCACGAC 240
TTTCTCTTAA CAGCTGTTGT AAAGTTTATT ACTTTATGTA CAACTGAACT TTTGTTTTAG 300
TTTTGATAAT AAAATTCTTT GGAACCTTAA AAAAAAAAAA NGN 343

SEQ ID NO:7507

SEQUENCE LENGTH:342

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08749

SEQUENCE DESCRIPTION:

GATCCAAGTG CTTNTTTGGT ACCAAGAGAC CCGGNTCTNT GCCAGCATAA ACCACTCACA 60
CCCCAGGGGG ATGAGCTCTC TNAGCCCAGG ATTCTGGCAA GGGAGGTGAA GAAAGTGGAT 120
GCGCAGAGTT CGGCTGGGGA AGAGGACGTG CTCCTGAGCA AAAGCCCATC CTCACTCAGC 180
GCTAACATCA TCAGCAGCCC GAAAGGTTCT CCTTCTTCAT CAAGAAAAAG TGGANCCNGC 240
TGTCCTTCCA GCAAAAACAG CAGCCCTNAA TAGCAGNCCN CGGTCTTTGG GGAGGNGCAA 300
AGGNAGGCTC CGGTTGCCCC AGATTGGCAG CANNATTATN AN 342

SEQ ID NO:7508

SEQUENCE LENGTH:369

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08750

SEQUENCE DESCRIPTION:

GATCAAGCAA TTAATCTTCT GTAGAACCAA AATTNACTGT AATAACTTGG AGCAGTACTT 60
TATACAACAA GGAGGAGGAC CTGATAAAAA AGGACACCAG TNCTCATGTG TTTGTNTTCA 120
TGGTGACAGA AAGCCTCATG AGAGAAAGCA AAACCTGGAA AGATTTAAGA NAGGNGATGT 180
AAGATTCTNG ATTTGCACAG ATGTAGCTGC TAGAGGNATT GATATCCACG GTGTTCTTCA 240
TGTNATANNT GTCACCTGNC CCGATGAAAA GCAAAACTNC GTACATCGAA TTGGCAGAGT 300
AGGGTGGAGC TGANGGATGG GTCTGGCAAT TNCCCTNGTG GCACCGAAAN NGGACAGGGT 360
TTNGTACCN 369

SEQ ID NO:7509

SEQUENCE LENGTH:335

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08751

SEQUENCE DESCRIPTION:

GATCTGGCCA GAGGGGTGTT GGAGCCCAGC CCACCCACAT ACCAGTCAAG CTCTTAGGGG 60
 AGCAGAAGAA AAGCAGGAAG AATTAAATG TTTAATTTT TTTNAAATT GACTTTNCTA 120
 GTTATTAAAA GTTGCTTGTT TCAGCAGTGN TATTGTATAA NGACCATCTT GTAAGNTACT 180
 CCTGACATCT TGCTTTAGCA CATGTACAGT ACAGTTNCTN TGATAATGTG TTTGCCCTAA 240
 CTNCCCTGGC TTCNCCTTCA GCCCATCCNC TCTCCTCTAG NGCAGTTGGG TTGGAGGCTC 300
 NTTGAGGCAA GCNGCANCAT TGGNGGGGGT GCAGN 335

SEQ ID NO:7510

SEQUENCE LENGTH:270

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08752

SEQUENCE DESCRIPTION:

GATCCGACAC AGAGAACAGG AGGAACTNAG GCGACAGCAA GAGGGCTTTA AGCCAAACTA 60
 CATGGAAGAA AGAGAACAGG AAATNAGAAT GGGTGATATG GGTCCCCGTG GAGCAATAAA 120
 CATGGGAGAT GCGTTTAGCC CAGNCCCTGC TGGTAACCAA GGTCTCCTC CAATGATGGG 180
 TATGANTATG AACANCAGNG CAACTNTACC TGGTCCACCA ATGGGTACTG GTNCTGCCAT 240
 GGGACCAGNA AGGNGCCGCA ANTNTNGGGN 270

SEQ ID NO:7511

SEQUENCE LENGTH:85

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08753

SEQUENCE DESCRIPTION:

GATCCAGGA GAATCAGAAA CTCCAACATT TTGGAATCTT CAAGGGCACA TACTGAGAAA 60
 AAAAATAAAA TTGTTTATGA GCAA 85

SEQ ID NO:7512

SEQUENCE LENGTH:66

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08754

SEQUENCE DESCRIPTION:

GATCAAACTA TACGCTGTCT ACAAGAGACA CTTTAGATTT AAAGACACAA ATAGGTTGAA 60
 AGTAAA 66

SEQ ID NO:7513

SEQUENCE LENGTH:390

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08755

SEQUENCE DESCRIPTION:

GATCTTTTGT ACTGAGGTTT TTAACACTTT ACTTGGGTTT ACCAAGCCTC AACTGGACAG 60

EP 0 679 716 A1

5 ACCATAAACA GTCCACAGGC ACCGTTCTTG CCAGGCCCA ACCCACAGGG AGTCTNTCCG 120
 CAGAGCCTTC TTGGTGTTC CCTAACTGC CAGTGGCCTT TGCTCAGAGC CTCCTCCTGT 180
 GACATGTGAA CAATGAAGAG GCCTGCGCCT CCTGCCTTG CCGCTGCAA GCAAAGAAAC 240
 TGCCCTTAT TTTTAACTT TAAAAAGTAG CCAGATTAGT ANCANGACTG GCTGGCTTGA 300
 TGAGCAAAGC CTTTGCTCTC ACGGNAGGAG GGTAGGGTTT NGGNTGTACA ATGGTAACTT 360
 GCNNTGGGNA CCTTAAAAAG GGAGGTGNAN 390

10 SEQ ID NO:7514
 SEQUENCE LENGTH:212
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08756
 15 SEQUENCE DESCRIPTION:
 GATCACCTGA GGTGAGAGT TTGAGACCA CCTGACCAAC ATGGAGAAAC CCCGTCACTA 60
 CTAATAATAC AAAATTAGCT GGGCGTGGTG GCACATGCCT GTAATCCAC CTACTTGTGA 120
 GGCTGAGGCA GGAGAATCAC TCGAACTCAG GAGGCGGAGG TTGNAGTGAG CCACTGCACT 180
 20 GCCTGGGCAA CAGAGCGAGA CTCCATTCA AA 212

25 SEQ ID NO:7515
 SEQUENCE LENGTH:136
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08757
 SEQUENCE DESCRIPTION:
 GATCCACCCG NCTTGNGCCC CCCAAAGTGC TGGGATTACA GGTGTGAGCC ACTGTGCCCC 60
 30 GCCGAGTTAA ATATATTCT AACATAGTAA AAAAAAAG GTANGTTNCA TTAAATAAAT 120
 CCNGGAAGTN CAAATN 136

35 SEQ ID NO:7516
 SEQUENCE LENGTH:160
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08758
 SEQUENCE DESCRIPTION:
 GATCATGAAG ATGGACAGAA CAGACACTGT GGCAATAAGA TACCAAATTG TAAACAGGAC 60
 40 CTAAGGCCAT GCCAAGCAAG GGTAAAGTCA TGTAGAGCCC GCCTTCATGC CCCGCCTCCC 120
 CTGCCCCCAA CTTATGAATA AACTATGTTT TAACTGCAAA 160

45 SEQ ID NO:7517
 SEQUENCE LENGTH:355
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08759
 SEQUENCE DESCRIPTION:
 50 GATCTGGAAC TTGAAGATGC CATTCATACA GCCATCTTAA CCCTAAAGGA AAGCTTTGAA 60

55

EP 0 679 716 A1

5 GGGCAAATGA CAGAGEATAA CATAGAAGTT GGAATCTGCA ATGAAGCTGG ATTTAGGAGG 120
 CTTACTCCAA CTGAAGTTAA GGATTACTTG GCTGCCATAG CATAACAATG AAGTGACTGA 180
 AAAATCCAGA ATTTTCAGATA ATCTATCTAC TTAANCAATG TTTAAAGTATG TTTTGTGTTG 240
 CAGACTTTTT GCATACTTAT TTCTACATGG TTAAATCGA CTGTTTTTTA AAATGNCACT 300
 TATANNTCCN AATAANCTGT TAANCCNGGN ANANGGNNTT GTNTTNGTGN GGNTN 355

10 SEQ ID NO:7518
 SEQUENCE LENGTH:77
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08760
 SEQUENCE DESCRIPTION:
 15 GATCTTCATT TTCCTGTTCT GTATTCTGCT ATGAAGTTCT CTGTTTTTCA AATAAAATT 60
 ATGTGTTAAA TAACAAA 77

20 SEQ ID NO:7519
 SEQUENCE LENGTH:20
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08761
 SEQUENCE DESCRIPTION:
 25 GATCATCTTG GAACTGCAAA 20

30 SEQ ID NO:7520
 SEQUENCE LENGTH:247
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08762
 SEQUENCE DESCRIPTION:
 35 GATCGGAGGC TGCAGTGTGA CAGTGCCAGC CAATGTGCAG AGGTGGATGA GGTCTTGTTA 60
 AAACCTGGCT CCTTTTAAACA CGGCCCTCAA GCTCCTTAAG TNAATTGCCG TAACTAATTT 120
 TAAAGGGTTT AGATTTTAAAG AATGGTGCTC TTTCATGCCT ATNATCAGTA AGGGGACTTG 180
 TATTAGAGTC AGAGTCTTTT TATTAGGCC AGTTGTCAAG TGTCAATAAA AGCATCATGT 240
 AATTAAA 247

40 SEQ ID NO:7521
 SEQUENCE LENGTH:164
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 45 CLONE:HUMGS08763
 SEQUENCE DESCRIPTION:
 GATCTTAATA TTGACTAGTT TCACATCCAG GTTTCTAAGA AATGATAAGA TACTTCACTT 60
 TTCCAGAGTG AAATGTAGGA GGGAGCACAT TCTAAGTACA GCTAAAAATT TAGCTCACTG 120
 TAACACAGTT TCACTCTCTG AATAAATAAA GCAAAAAACA CAAA 164

55

EP 0 679 716 A1

SEQ ID NO:7522

SEQUENCE LENGTH:110

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08764

SEQUENCE DESCRIPTION:

GATCTGCCTG CGAAGCTCCC CACAACACTG TCCCTGGAGA CCACCCATGT GGCAGACACT 60
 CAAAATCTGT TGTATTGCT AAATAAATTA ATATGGACAA GTTACCCAAA 110

SEQ ID NO:7523

SEQUENCE LENGTH:181

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08765

SEQUENCE DESCRIPTION:

GATCAAAATTG TTCATGCCCTT GGGATTTTT CTCTATAAT TTGGATATCT TTNTCCATTG 60
 CTCATTCTT TATTGAAGTT GCTTTCTTAA AAATTGATTT AACTTTGTCC TTGGTATCTT 120
 TAGTTCAGTC CAGAAATNAT TAATTGTGAT GTGATTAAAT TCATTTTTTG GTCTGGTGAA 180
 A 181

SEQ ID NO:7524

SEQUENCE LENGTH:175

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08766

SEQUENCE DESCRIPTION:

GATCTGAATG GTTTTAATAA GGGGCTTTCC CCCTNCTTCG CTCTGCACTT CTCCTTGCTG 60
 CCATGCGANG AAGGATGTGT TTGCTTCCCC TTCTGCCATG ATTGTAAGTT TCCTGAGGCC 120
 TCCCCAGCCA TGTTAAACTT TGAGTTAATT AAACCTCTTT CCTTTATAAA TTAAA 175

SEQ ID NO:7525

SEQUENCE LENGTH:362

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08768

SEQUENCE DESCRIPTION:

GATCTGAAAA ATNCTTTTTG TCCTCATTGT TGCAGTTTCA ATTGTAATCC ATTGCATCTN 60
 ATTTTCTTGG GTGTTGGCAC TGTAATATAT TAAAAAATAA TTCAGTGCTC AGTATTGTAA 120
 CAACTGTCCC TACTGAATAT TCCTTTTCAT AAATACTTGC TACCACAGGG AAATTAAGTT 180
 TTCATATAGA ATAAC TAGTT TCAGTAGTAA CCATTGAAGA NTAANCNTG TGGTTCANGG 240
 CAGATATTTT TCTGGAAAGT TTTCTCTATT GTANAATTTG TNGTATATGG CTATGCTGAC 300
 TATCNTGGAT NCTGTCATGG GACATGCATT ACCACANNTN CNNGCCCCTT TCTGTGGTNN 360
 NN 362

SEQ ID NO:7526

EP 0 679 716 A1

SEQUENCE LENGTH:306

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08769

SEQUENCE DESCRIPTION:

GATCCCATGG ACATTTGGGG AAAGGGCTCC TTGGGCTGCT GGTGAACTTC TGTGGCCACC 60
ACCTCCTGCT CCTGACCTCC CTGGGAGGGT GCTATCAGTT CTGTCCTGGC CCTTTCAGTT 120
TTATAAGTTG GTTTCAGCC CCCAGTGTCC TGACTTCTGT NTGCCACATG AGGAGGGAGG 180
CCCTGCCTGT GTGGGAGGGT GGTTACTGTG GGTGGAATAG TGGAGGCCTT CAACTGATTA 240
GACAAGGCCG GNCCACATCT TGGAGGGCAT CTGCCTTACT GATTAAAATG TCAATGTGAA 300
TCTAAA 306

SEQ ID NO:7527

SEQUENCE LENGTH:76

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08770

SEQUENCE DESCRIPTION:

GATCTTTTAG TTATCAAACG GTTAAATACA TTTTAACTTT CAAATTTTAT GAATAAAGGA 60
GATGAATCCT GTTAAA 76

SEQ ID NO:7528

SEQUENCE LENGTH:74

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08771

SEQUENCE DESCRIPTION:

GATCTGAAGT CTGATTGTGT GTACGTTTCG GCGTGCGTTA GTCCCTGCCA CGATTAAAGA 60
CTTAGACCGN CAAA 74

SEQ ID NO:7529

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08772

SEQUENCE DESCRIPTION:

GATCGCGCCA CTGCACTCCA GTCTGGTGAT AGAGCAAGAC TCCATCTCAA AAATAAAAAA 60
TAAAATGTTG GNTGTGGGGA GCCAGGCCTC TCACAACTGA AA 102

SEQ ID NO:7530

SEQUENCE LENGTH:312

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08773

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCGAATCC AGGCCCTGGG GCTTCANTTG CCAGACCCAC CATTAGAGAG TGAAGATGAA 60
 GATGAGGAGG GAGCTACAGC GTTGAACAAC CACAGCTCTA TTCCCATGGA CCCAGAACAT 120
 GTAGAGCTGG TGAAGAGGAC AATGGCTGGN GTAAGCCTGC CTGCGCCAGG GGTTCCCTGCC 180
 TGGGCTCGGG AGATATCGGA TGCCCACTGG GAAGATGTGG TACAGAAAGC CCTCCAAGCC 240
 CGGCAGGCAT CCCCTGCCTG GGAGTGACCA CAGTGAGAGC TGCCTTATAT TCCTACATTC 300
 CAGGCCAGAA CN 312

SEQ ID NO:7531
 SEQUENCE LENGTH:186
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08774

SEQUENCE DESCRIPTION:
 GATCTGGACT GAGGACCCTG CTAATCCCCA AGCCAGAGCC CATCAGCCAG GCCTGCTGTG 60
 AGCCACCTGC CTGTGGAGTG CTGAGCTCAA CCAAAGGCTG GCAAGCTCTG GGCTCATT 120
 AAGGGATTCT GATGAGCCGA TGGGCCCTGG AGGCAGCCCA TTAAAGCATC TGGCTCGTTT 180
 TTGAAA 186

SEQ ID NO:7532
 SEQUENCE LENGTH:390
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08775

SEQUENCE DESCRIPTION:
 GATCACATTG CCATTCTCC CCTCCAGAGG TAACAATTAT CCACAATTG ATGTTTATCA 60
 TTCCTGTGTT GTTGTACTTT CACTGTGTAT AACCTAANNC NTCTACTNTT TAGTACTGTT 120
 TTATATATTT TNAAGCCTCA TACTTGCTCA TTCTACAGCT TTTTCACTC ATTATTGTAT 180
 AATTATATCT GANGCNCTCG TTCATTAATT TTAGTCCNGT GTAGCAGAAT TCAATTACGG 240
 GAACTACCAT AATTTATCTG TNCTCCAGTT GAAGGCATGA NGTTGTTGCC AGTTTCTGTA 300
 TTATAACCAC TGTAAGGGGA CCATTCTTCT GCNTTGGGCT CACTGCGGGT TACCNAAGNC 360
 GGTNCCNCAG GATAANCCCC ATTTGGGNTN 390

SEQ ID NO:7533
 SEQUENCE LENGTH:378
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08777

SEQUENCE DESCRIPTION:
 GATCTAGCAT GTGGATTTTA AAAGATTGCT CCTCATTAAC AAGAATAACA TTTAAAGGAG 60
 ATTGTTTCAA AATATTTTNN CAAATTGAGA TAAGGACAGA AAGATTGAGA AACATTGTAT 120
 ATTTNNCAA ANCAAGATGT TTGTAGCTGT TTCAGAGAGA GTACGGTATA TTTTGGTAA 180
 TTTTNTCCAC TAGCAAATCT NGATTNGTT TGATAGTGTG TGGAATTTNC TTTTGAGGGA 240
 TAAGACCATG GGANANTTGT GGTAAAGACT GTTGTNCCC TTCATGANTN CTTCTGAAGT 300
 TGCCNTCAGT TTTNCTAATC TCCTGTGAAA TGCCTAGGTT TTGCGCCTGT CCCACTTTT 360
 NTTTGTGGGN CTTATNTN 378

SEQ ID NO:7534

SEQUENCE LENGTH:175

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08778

SEQUENCE DESCRIPTION:

GATCATTGA GTGAAAAA GGTACCTGTN CAAGCAAGCT CCTGGACACC ACAAGAAGGA 60
GGAATTATTT TAAAAGCTGT ACTCTTAAAT TGTNAGTATC TTAAAAATCA GTTGTGAACA 120
ATGAAGGATT TGAAAGAGCA TTGACTTTGC CACTTAAAAG TATTCTAAA ATAAA 175

SEQ ID NO:7535

SEQUENCE LENGTH:159

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08779

SEQUENCE DESCRIPTION:

GATCAAGGTG AATTTTTTGT ATCACTGCCT GTGAAATCT ATCCTCATCA GTNATTGCAT 60
TTTTCCCTGC CTATACCTGT GTCCTTTTT NTNACTGTGT TTTCAGTCAC TTCCTTTCTG 120
TNAAAGGTG CTTAGCTTTT NTTTTNAANA TTTGTTGTN 159

SEQ ID NO:7536

SEQUENCE LENGTH:304

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08780

SEQUENCE DESCRIPTION:

GATCCAAACC CACAGTNTTG TCCTGGAGGC AGCAGGGGTG AAGGTGGAGG GTCCAGGGCC 60
ATGAGGAGCC CCCTTGCCAT CAGAGCCTGG CCTAACCACC CTCTTCTCTA CTTACACACA 120
CATGCATTTT ATAATAGCTC TGACCCAACC TGGCCACTCT GCAGAGACTG GGACAGACAG 180
GTGCAGGCAA TGGGCCCTCC CACACCCAGT CACCTACAAG GAATTTTCAA ATCCACTTTT 240
AAAACAGAAA CCGGTAAATG CGCCGTATTG TATATTTTAT TTAAATAAAA AAAATTCAG 300
CAAA 304

SEQ ID NO:7537

SEQUENCE LENGTH:110

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08781

SEQUENCE DESCRIPTION:

GATCCACCCT TCCTGGGCCT CCCAAAGTGC CGGGTATTAC AGTCATAAGC CACCACACCC 60
GGCCTAACAT GCATTTTTTT AATCAATAA ATATTTATTG AGCACCTAAA 110

SEQ ID NO:7538

SEQUENCE LENGTH:160

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08782

SEQUENCE DESCRIPTION:

GATCCCCTCC CCTCCTGCTT TTCTGTATTT TTTAAAAATT ATTTTGTTTT TAATTCACAA 60
ATATTGTATA TGTTATATGG GGTAGAATGT GATGTTGATA TATGTTTAAA ATGTGGAATG 120
ATTAAATCAG GCTAATTTAC TTTTTTNCC NAAAAGGAAA 160

SEQ ID NO:7539

SEQUENCE LENGTH:219

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08783

SEQUENCE DESCRIPTION:

GATCCACCCA GTTGCTCAAG TAAAAACCT GAGAGACACC TTACGCCATC TGGGAACCTG 60
TTAGAAATTC TAAACCTCA TTCTATACCT GCTAAATCAG AAAATGTAGG GATTAAGTCT 120
GATTATTGTG GTTTTCGCAA GTCATCCNGG TGATTCTGAT GCATGGAAAG TTTGAGAACC 180
ACTGGTTTAG GTTATTAATA GTTCTGTCT CCCTATAAA 219

SEQ ID NO:7540

SEQUENCE LENGTH:355

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08785

SEQUENCE DESCRIPTION:

GATCAGAGAA GACTTTAAAA CTCTTGACTT AATTGAGTAA ACTCTTCATG CCATATACAT 60
CATTTTCATT ATGTTAAAGG TAAATATGC TTTGTNAACT CAGATGTCTG TAGCCAGGAA 120
GCCAGGGTGT GTAAATCCAA AATCTATGCA GGAAATGCCG AGAATAGAAA ATATGTCACT 180
TGAAATCCTA AGTAGTTTTG ANTTCTTTG ACTTGAATCT TACTCATCAG TAAGAGAACT 240
CTTGGTGTCT GTCAGGTTTT ATGTGGTCTG TAAAGTNAGG GGTCTGTTT TNGTTTCCTT 300
ATTTTGAGGT AAGAGTACTG CTNGGTGGTC GGGGGGGTTA TATNNTNCCC TTTTN 355

SEQ ID NO:7541

SEQUENCE LENGTH:314

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08786

SEQUENCE DESCRIPTION:

GATCAGGTTT CCCCTCAGAA CCTGTGTTGC CTGCCTGCTG TATCTTCCAT GTCTTTCTTA 60
TTCAACTTCT AGAAGTAGAG AAGGTTGGGA CTTGAGTGTA GAAGAAACAT CAGAATAATT 120
TCAAAAAACA GGAAGTTGGA ACTATAATTT TAAATTATT GTATTGTTTT TACGGATTTT 180
ACATGTATAG TAAATATTA ANNTTCATCT CTTGCAGTTC ANTAAAAGCT ATAGTATAGA 240
TTTTATTTT AAGAAGTTTA TATAATNCTT TTGTGAGCCA ATATGTAAAA CTNGAATATT 300
TATTTANCTT ANTN 314

SEQ ID NO:7542

SEQUENCE LENGTH:298

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08787

SEQUENCE DESCRIPTION:

GATCACAGAG AAAGTGATTA CAGACATTGC TGGGGTAATA CCAGCTGAGA AAATTGATGG 60

AGTATTNCT GCCTGTNAGA GTGGCTCTTT TGACAACTA GANGCTGTGG TCAAGGATTT 120

AATAGATGAG GGTCATGCAG CAACTCAGCT CGTCAATCAN CTCCATGATG TGGTTGTAGA 180

AAATANCTTA TCTGATAANC AGAAGTCTNT TATCNCAGAA AACCTTGCCG AGGTTGCCAA 240

ANGCCTGGCA GATGGTNC TGTTCCATTT GCANCTCATC NGCCTTTTNG CCCTGNGN 298

SEQ ID NO:7543

SEQUENCE LENGTH:32

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08788

SEQUENCE DESCRIPTION:

GATCAAAATT AAAGACAGTT AAAAAGGTGA AA 32

SEQ ID NO:7544

SEQUENCE LENGTH:249

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08789

SEQUENCE DESCRIPTION:

GATCATCATT TATTGCATCT CATACTAAA TTTNNTAAAG TTTGGATTGG GACTTTTNAG 60

GTCCTTTTGG GAGGGCAAAG GAAGTGCCAG CTTCTNTGGG GAACTTGTTT TTAAATCCAA 120

AGACTTGAAC CACATTCCCT GCACATGANC ATGTTTGCTT TTATCCCTTC TCTATTGTN 180

TCCTACCCAT CTTAGTACCA TTGTGGTTAT AANCATCTGC ATTTNNTAGA AGCATTTNAC 240

CCATTNNN 249

SEQ ID NO:7545

SEQUENCE LENGTH:257

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08790

SEQUENCE DESCRIPTION:

GATCATATGG AATGTACTAT TTTGTAATGT CTTTTTTCAT TTTACAATGT ATTATCAACC 60

TTTTCCCTCT CAAAAATACA TTGTGAATGA CTGCATAGTA TTCACCTTAT GANTATTTAA 120

TTCATTTCAC AGTCCTTCTAT TGTNGGACCA CTNACATTGT ACCAAATGTT TTCCTTTGGT 180

TTATTCTTTA ATGTATTAGT ATTTTACTGC TGGTCACTCA TGGAATCCTG CAGCTTTANT 240

AAAAAGCAAG GATGAAA 257

SEQ ID NO:7546

SEQUENCE LENGTH:158

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08791

SEQUENCE DESCRIPTION:

GATCGTGCCA CTGCACTCCA GCCTGGGCGT TGCAGTGAGA CTCCGTCTCA ACAACAACAA 60
AAAGGTGGAT ACATGTCAAA AGGGCACAGG AGCCACTTGA AGGATTATAC TTGCTAAATC 120
TGTGTCAATT ATCAAAATAA ACTGGTAGCA ACGTTAAA 158

SEQ ID NO:7547

SEQUENCE LENGTH:128

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08792

SEQUENCE DESCRIPTION:

GATCAAAGGG ATGAGCAACA GGGACTTCTG CCACAGTGAC AATGGAATTG TGTTGTGCCT 60
TACTTCAGAG GTGGTCTCTN CTTTCTTGTA ATAAAAGCAA TATTATGCG GAAAGCAAGC 120
AGCTCAAA 128

SEQ ID NO:7548

SEQUENCE LENGTH:205

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08793

SEQUENCE DESCRIPTION:

GATCACATCA AGCTAAAAA CTTCTACACA GCGAAGGAAA CAAAGTGAAC AGAATAACAT 60
GGGAATGTTT TCTGTAATTT AGTAGTAACT GGCAATAGTT TACAAACACA TTTTGTGTAT 120
ACTGCTGTCA TTGCACTGNT TACCTTCTGT TGTAAGTGACT TTGTTCTATT AGTCCACTCA 180
ATTAAAAATAT TTGGTTTTGT TAAA 205

SEQ ID NO:7549

SEQUENCE LENGTH:372

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08794

SEQUENCE DESCRIPTION:

GATCTTATTT TTAATGTAGT GAGGATATTA TTAAACTTT TATTTAACT GGAAATGTCC 60
TGAAACACAT ATTTAAAAA TTGGGATACA GTGAAAGAAA AATCAAATT TTAATAACAT 120
AAAGATTTC TAACTTTATG TTATTGANCA CTTACTCACT AGAAGTGAGT TCITTAGAAA 180
ANTACAGTGA AGGACTCAGT TCAGTCTTGT TTTATCAGA GTGATAATCA TCCTGTTTCA 240
CATCCCAATA CTATTTTGAN ATTCTAAACA ATGGAACCCA AANTNCCAAT AANTATAAGG 300
TTATGCCTTC AATATATTCC TATACANTTC TGTAACCATG GTTTANNATA CACAAGCTTA 360
NNATACCATG GN 372

SEQ ID NO:7550

EP 0 679 716 A1

SEQUENCE LENGTH:97

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08795

SEQUENCE DESCRIPTION:

GATCCGGTNG TCTAAATGCA TTCATATTTT TATGATTGTT TTGTAAATAT CTTTGTATAT 60
TTTTCTGCAA TAAATAAATA TAAAAAATTT AGAGAAA 97

SEQ ID NO:7551

SEQUENCE LENGTH:244

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08796

SEQUENCE DESCRIPTION:

GATCTGGGTT TGGCATTAGA AGTATTTTCAT AATTTTGGTT TTTNATTTAG GTTTCCTCAA 60
CATCTGTAAA GTGATTGATT AAATTAGAGG AGGCGTGTAG AATAAATCCC AATCCCATTG 120
CAACTGGCAG AGCATTATAA NTNTTTATAA ATNCAGTTAC AACAAAGGAG AGGNTCTACA 180
TTCTTCAAAA AANAAANTTG GCTTACCTGT TTCANCTTN GGTGGCATT NNCTGCCATT 240
NGTN 244

SEQ ID NO:7552

SEQUENCE LENGTH:364

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08797

SEQUENCE DESCRIPTION:

GATCTGGGAA TTACCCATCA TCATTAAGCA ATGAAACAGA CCGGCTGGTG CACTGGTGCC 60
ACGGCGCCCC GGGGGTCATC CACATGCTCA TGCAGGCGTA CAAGGTCTTT AAGGAGGAGA 120
AGTACTTGAA AGAGGCCATG GAGTGTAGCG ATGTGATTG GCAGCGAGGT TTGCTGCGGA 180
AGGGCTACGG GATATGCCAT GGGACTGCTG GCAACGGCTA TTCCTTCCTG TCCCTTTACC 240
GTCTCACGCA GGATAAGAAG TACCTCTACC GAGCTTGCAA GTTGCAGAG TGGTGTCTAG 300
ATTACGGAGC ACACGGGTGC CGCATTCCTG ACAGACCCTA TTCGCTCTTT GAAGGCATGG 360
CNAN 364

SEQ ID NO:7553

SEQUENCE LENGTH:129

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08798

SEQUENCE DESCRIPTION:

GATCTGTGTG TCTCTGTTTT GAGTTTTTCC TGTTTATTTT GAAAAGTACT GTTGGTCAAG 60
ATAATTGGTC AATAATCCAT GTTGGTTTTA AAAAAAGCA TTTTAACATT AAAAATATTA 120
CAGTATAAA 129

SEQ ID NO:7554

SEQUENCE LENGTH:316

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08799

SEQUENCE DESCRIPTION:

GATCACATTT TNATTTTTTN TTCTCCACAT CAGGATAGTT TACTGAAGCA CAATCTCTTA 60
TACTAGTGGG ACAAAGGGA GAAAAAGGAA GCAAGATAAA TGGGTATGTA GGATGAAGGG 120
TTATTTAAAA TGGAACTAAA GATAGAAGGA GGACTGTAGG AAGANATGGA ATNNTTTANN 180
TNTGAGGAAA GATATCTNTG GTAGACATGT CCTTCCATGA CTAATTCTA ATTGTNACTC 240
ANCACACATT GAGGTATGGN CCCTCCTCAG TGACTTTNAC TAGCTCAGAN ACGTACTCCC 300
CCACCANCCC CACCTN 316

SEQ ID NO:7555

SEQUENCE LENGTH:365

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08800

SEQUENCE DESCRIPTION:

GATCAGTGGA ATTCTTGTTT TGATGATAAC CTTATTAATT GAAATNTTTT ACTGATGTGG 60
CTTTAAAAGA GGTATATNTT GTATATGTTT AGAACTCTCT GATTTTNATG AATTATATGG 120
GAATGAGAAA CAGAAGAAGT GGTATTTNCT GCGGAGTAA ATAGGCAAGG TACCCAGTGA 180
TAACACCAAC CAAACCACTC CTATCTGCAT GATTCTGAAC ATCTGGATGC CTGTGGTTTT 240
ACTGTGTATA TNTNATTTTT AATATATTAC CTTTGTGGAT NCATTTAAGG TCTACTCAA 300
NGTANCACTG TCAAAACCAC TAATATGTAT GTNAAANTTG TNCTGTNTAC TACATTACNG 360
TNCAN 365

SEQ ID NO:7556

SEQUENCE LENGTH:349

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08801

SEQUENCE DESCRIPTION:

GATCTTGAGT AACTGAACTT ATTTCCCTTA AGGTATAAAA ATTTAAATAA CCTGTATATA 60
TTTGNTAACA NCTTTATNAG GGAGGTAAAGT NACTTACAAT ACATTGCACA TATTTAANGT 120
ATAGANTTCG ACGAGTTTGG ATGTATGTTT GCACCTGTGA AACCATCACA ACAAACAGTG 180
AGCATATCTN TCACCCCTAA NNGTTTCCTC CTGTCCCTTG GTAATCCCTC TTTTACCTGT 240
CCCACTTCTG TTCCTCAAGA NCCAATTACC TGCTTTNNTN ACTGTTAATG TACGTGAGTT 300
TACATTTTGG AGAGTTTTAT CCAAAGGGNA TCATGANGTA TGTNCTCTN 349

SEQ ID NO:7557

SEQUENCE LENGTH:369

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08802

SEQUENCE DESCRIPTION:

GATCTNATCA ATCTAGCGGG AGAGACAGGA TAACCTGTCC GAAAGTATAG CGCCACTATN 60
ACTCCGCCGG AAAAATTACT TAAAAATCG CCAAAAATTA CTTGGAGCAA AGGGCAGTCG 120
GCGGANNTTCG CCAAGGCTGG CGCAGTCGGT TTNACCTGT AGCAGAGAAC CNGGNCCTGGA 180
GAACAGCCTC ACTTCTTTNA TTGANTACTT ACATAATGCA TTGGAACATG ACATGAGATT 240
AAGGTTTAAT AATGATAGAN TGAAGACCAC AATAAAGAG ACCTCTACTT AGCTCAGCAA 300
TTCTTACCTT TCTTACCTAT TTGATGGAGG NTGTCTTTG ANAGGTGTNC TGCAGGGNCC 360
AAANTGTTN 369

SEQ ID NO:7558
SEQUENCE LENGTH:290
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08803
SEQUENCE DESCRIPTION:

GATCTTGAT GCCAACTTT AATCTGCTTT TATGTTTCA GGCTGAAGGT GTGAAAATCC 60
TAAGAGGATT TCATATTGAA TATGTGTACA CAATCTTAAC TATCGTGGTG GAAAACATAC 120
TACTATAATT NATTATTATA TCTNCCAGAT AATGTTATTC ATTTAGAACA AATAAGGTAT 180
ATTTNTNAGA ATCANCTTG TAAGCACTAT AANNCTTTN ATAAGTTATA AGGTCTATGA 240
TGTGTTTACT TTAANNCTTG CTGTTAANAG CAACACGTAT TANNTATGTN 290

SEQ ID NO:7559
SEQUENCE LENGTH:55
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08804
SEQUENCE DESCRIPTION:

GATCTGGATA AATTTTCATT TCTACTTAAT TAAAACTTCC TATGTAAAAT CAAA 55

SEQ ID NO:7560
SEQUENCE LENGTH:109
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08805
SEQUENCE DESCRIPTION:

GATCCCGAAT CCCAGAAATA ATTCATAGNG CACCTATCAT GACTATTTAT TTAATCTCAG 60
AAGCTGAATC TGTACGTATT TTTCTCCAGG TCATCAGCTT TGGGNNNNN 109

SEQ ID NO:7561
SEQUENCE LENGTH:40
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08807
SEQUENCE DESCRIPTION:

GATCCTACTC TCTTATTAAT ATCTTGAGTT TATGTTCAAA 40

EP 0 679 716 A1

SEQ ID NO:7562

SEQUENCE LENGTH:338

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08808

SEQUENCE DESCRIPTION:

GATCTGCCGA CCTCGGCCTC CCAAAGTGCT AGGATTACAG GTGTGAGCCA CCGCGCCCAG 60
 CCATAACTTT NCTCTTTTCT CCATTAGCTA AAAGATAATA GTAAACGTA TATTGAACA 120
 CTTAATTTTC TCTATATATC TTTTNNAGGAT TATATTAGT GTATTTCCTA ATTTCTCTAA 180
 AATGATTATC ACTTCTGTAA AGAAGAAAAC AATACTACTG GTATTGCATT TGGAAATATT 240
 TTNCTATTAA NNTGTCTCAT TTCCTTTNCA TGTATGCACA TACATGTNNT TNGTATAGCT 300
 CCTTTNNTCA AAANNTATTG TNGGGTTATT ATTTANNN 338

SEQ ID NO:7563

SEQUENCE LENGTH:338

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08809

SEQUENCE DESCRIPTION:

GATCTTGTGG TCAAGAGCAA TCTGAATCCA AATGCAAAGN AGTTTGTCCC TGGGGTGAAG 60
 TACGGAAATA TTAAAGTAGA CGGGGCCCTC TTTTGGTGGA TGTAGCACA TTNCCACACT 120
 GTGAAGGCAG TATTAGAAGA CTTAATTGTA AAANCNCTCT TGCACTGTG TTACACTTAT 180
 GCATTGCCAA AGTTTTNTN AGTCTTGCAT GCTTAATAAA NGTNCTGAGA CTGTTACTAA 240
 GTAAAANGCT GTCAANCATT TCCTGANAAT AGANTTGGCC CCATGGCTTG ATGTGAAGAC 300
 AGCAAGGNAA GANGCACCAG TCAAGTTGTG ANCAAGNN 338

SEQ ID NO:7564

SEQUENCE LENGTH:324

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08810

SEQUENCE DESCRIPTION:

GATCCCTGCC ACAAGTTCCT TGGGCAGTGG CCATGTCACC ATTGAGATGA AGATATACAA 60
 CAGAAAATAG TGGCTGTGTT TGGAAGCTTC AGCCCTGCAC ATTTGAACTA GTCACCTCTC 120
 CAGACTTGCG TGGGTGAGT CTTTCTGAGT AGAGGACTTG CTGGTAAAGG GGCAGATGCT 180
 TTTTATTAGT ACTGATAAAA CAACTGAGG GAAACATCCC TCTTAGCTGG GAACTTTTA 240
 CTCTTCAGGA GCTTGGCATC ATGGACTGTT AATGTATGTG ATTTTCCCCC TATTTTCTCT 300
 CTCCAAAATG ATAAAAACAA TAAN 324

SEQ ID NO:7565

SEQUENCE LENGTH:318

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08811

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCCCACTA CGAAACGCTC CAGAGGCTTC GGTTCGTCA CGTTCGCAGA CCCAGCAAGT 60
GTAGATAAAG TATTAGGTCA GCCCCACCAT GAGTTAGATT CCAAGACGAT TGACCCCAAA 120
GTTGCATTTC CTCGTCGAGC GCAACCCAAG GTGTTCTAGC TGAGCGTTTA AGAGCATGGA 180
CTCTGGAACC AGACTTTGAA TCCTTGCTCT GCCACTGCAG CTGTGTGACC TTGAGCAAGC 240
TATCTAAATA TTCTGTGCCT TTGTTTTGTC ATCTGTACAA TGGAGATGAT GATGGTATCA 300
CCTTCATGGG GTTGTGAN 318

SEQ ID NO:7566
SEQUENCE LENGTH:313
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08812

SEQUENCE DESCRIPTION:
GATCTGAGAC TCAGGAACCT TGGCCCCTTT GTCACCTACA ACTGTGTGTG AACAGGACTA 60
ACAGTTTGA CTGAGAGCAC TGANGCTGCT GTGTGTTGTG CATATAACTT AATGCTGTGT 120
GTTGTGGCTT GCACTGCTGT GGGGGCGGGG AGGGCAGTGG TGGGAATGG CTGGCATGAA 180
GCTTGCTTGA GCCAATGCTA TGCTTGCTGG GCTTTGGCTG ACTGGCTTTG GGCCACCAAC 240
TGTATTGCA TAGTGATGGC TTGGAAGTGT CCATAGAAGG GATTGCAATA AAGGTGTGTC 300
TTCCTTCTAA AAA 313

SEQ ID NO:7567
SEQUENCE LENGTH:316
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08813

SEQUENCE DESCRIPTION:
GATCTTGAGT CAGAGAGGAT TGGAAGTGCT TTCTCCTCCA CCCAGGTGAG GTCAGGGGAG 60
CTTAGGTCTT AGGGAGATGG CAAGTTGAGG TATGAAGGGA AGCTGGGGCT TTTGGAGCTG 120
CCGAACAACCT GAGGGACCCA GTGCGCTTC CATCCGCAC TAGTGAATAG CGCCCCCTCT 180
TCCCCGAAA ACGAGGTGCG AGAGGAACAA TTCCCACGCT GGGGAAGGAC TTGTCTCCTT 240
TTCTGTGAAA ATGCTTTGTA AAAAGTTGTT ATTGTTTGCA TAGAGCAGAT TCTTGAGAAA 300
AACTGTTTTG GACCAN 316

SEQ ID NO:7568
SEQUENCE LENGTH:316
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08814

SEQUENCE DESCRIPTION:
GATCCCCGTC TGCTGACCAG CTAAACACCA ATTTCTTCCT GCTTTTCTCC ACTTGGTTTG 60
GAAAAACACA CAGTTTTAG GCTCCATCTG TTTGGAGAAA ATACATTCTG AAGCATCCCC 120
AATTCACCTT CTA AAAAATC ATGTGCAGGT TTGATAAACA CCAGAACAGA AGACAGTGAT 180
GCTGTATTAT TTTAGATTTA TTACATAGAT TTGGAATTCA CTTTTTTCAT GACCTAGAAA 240
AAAACATTCC AGTGTTCANC TGTTTTNTAT TATTANGGGG CTTTNNATT GTGAACCTTCT 300
GANGGCATGA GTGTTN 316

EP 0 679 716 A1

SEQ ID NO:7569

SEQUENCE LENGTH:226

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08815

SEQUENCE DESCRIPTION:

GATCTGGTGT ACCAGGCGAA GTGGTCCGAG CAGGCTGAGC GATACGACGA AATGGTGGAG 60
TCAATNAAGA AAGTAGCAGG GATGGATGTG GAGCTGACAG TTGAAGAAAG AAACCTCCTA 120
TCTNTTGCAT ATAAGANTGT NATTGGNGCT AGNNGAGCCT CCTGGAGAAT AATCAGCAGC 180
ATTGANCAGA ANGAAGAAAN CAAGGGAGGA GAAGACAAGC TAAANN 226

SEQ ID NO:7570

SEQUENCE LENGTH:306

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08816

SEQUENCE DESCRIPTION:

GATCAAGAGT TAAATAAAAA GCCCCAGGAC GAAACAAGAN GAGAGCACTT CATGCCCTGT 60
GGTACAAAAA AGAGCAGCTC TACTTAATGC AATTCCTCAT TCAGCATATA GCGAGACATT 120
TCTCCTGCCT CATTTGAAAG ACATCCAGC ACAGCATATC ACGCTGTTTC TTAAGTATTT 180
GTATNNNNNN GTACCTGAAG TGTAGCGAAA ATNCTACTAT GACTCTNCCT GGAATACACC 240
CACCTACCTT GANCCAGATT ATGGATTGGN TATGTCTACT TCTGGATGCA AATTTTNCCTG 300
TTGTTN 306

SEQ ID NO:7571

SEQUENCE LENGTH:304

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08817

SEQUENCE DESCRIPTION:

GATCCTGCGA GGGTGTCTATA ATACCTTGCT TTTCCATGCT TCCTGTATAT TTATCCATTT 60
CAGCACATCT GCAGTAGCAA TAACTNCTNA TTTNTAAATT TNCTTTTGTT GGGGGAGACA 120
GGCTTATGGC TGTCTGAGCA GCTGCTGTAG TGTAAGCAGT GAGGTTAGCA GTGGTTGTNA 180
GATTTNCTCA TTCCTGAGCA CCATGCTGTT GTGTCAGCAG TTGTAATGGA CTGTGTGGGC 240
ATACTTCCAG TAGGTGATGC TTGCAAGTAN GANCCAGCTG CAGTGGTAGC AGTAGGGTTT 300
GTAN 304

SEQ ID NO:7572

SEQUENCE LENGTH:30

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08818

SEQUENCE DESCRIPTION:

GATCTGTACA AATAAAATNC CAAGTCCAAA 30

SEQ ID NO:7573

SEQUENCE LENGTH:118

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08819

SEQUENCE DESCRIPTION:

GATCATCTCT CTTGGGTTT TNNTTAAAA AGGGGAATCT NCTATAAAGG TTCTNTTGCT 60
TCAAACCAAT GTCAAATAGA CTTNATTTTA AGAGTCATGG AATTACAGTG CAACCTTN 118

SEQ ID NO:7574

SEQUENCE LENGTH:53

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08820

SEQUENCE DESCRIPTION:

GATCTACCTA TACAGTCCTA CATTAGCTTC TAAAAATTTT GTCAGGAGGG AAA 53

SEQ ID NO:7575

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08821

SEQUENCE DESCRIPTION:

GATCCCGAGG CTTTGCTTC CTCTCGTCAG TTCTTTTGGT TGTGTTTTTT GTTTTTNTTT 60
NAANAACCTCA AAAAAAAAAAN AAAAGACTTG GAGGAAGGGA AA 102

SEQ ID NO:7576

SEQUENCE LENGTH:362

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08822

SEQUENCE DESCRIPTION:

GATCCTACTG ACAGCCATCG TGCAGGTGCT CAGCTGCTTC TNTCTCTATG TCTGGTCCTT 60
CTGGCTTCTG GCTCCAGGCC GGGCCCTTNA CCTCCTGTGG GTGAATGTNC TGGGCCCTG 120
GTTCACTGCA GACAGTGCCA CCCAGCACC AGAGCACAAT GAGAAACGGC AGCGCCGACA 180
GGAGCGGCGG CAGATGAAGC GGTATAGCC ATTGANATTG TGGCCACAGG CCACTGGGCC 240
CTGGGTGGCT CTGTNAGGGT GCACAGCCCC TCATGCCTGG AGCAATGAGG GTCTAGTCCA 300
GGGGCCAAAA GCAGTCTTGA GGGTATTGGG GTATACTTAT ACTCTATAGG GGTGTTTGA 360
AN 362

SEQ ID NO:7577

SEQUENCE LENGTH:109

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

EP 0 679 716 A1

CLONE:HUMGS08823

SEQUENCE DESCRIPTION:

GATCACTCAT ATAACATGTC ATTTTTTTGG TTCTGTTTTG GTTTGGTTTT TGCCAATNAT 60
TTTGTATAT TTCCAAAAA CTAATAAAA ATNATTTTAA TTTTNNAAA 109

SEQ ID NO:7578

SEQUENCE LENGTH:361

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08824

SEQUENCE DESCRIPTION:

GATCTTCACG GGGCTATTAT TTCAGTGACA AAATCCAAAT GCCCCTCTTA TGTGGGTATT 60
ACAGGAATCC TTCTACAGGA AACAAAGCAC ATTTTCAAAA TTATCACCAA AGAAGACCGC 120
CTGAAAGTTA TCCCAAGCT AAACGCGTG TTCAGTGTGG AAACCGATGG CTTTATTTC 180
TACATTTACG GGAGCAAATT CCAGCTTCGG TCAAGTGAAC GGTCTGCGAA GAAGTTCAAA 240
GCGAAGGGNN CGATTGACCT GTGANTTCTT TGCCGTCTAA GGCAGTTGTT TATGACAGCT 300
GAAACTGGA CACTCCCTAA NTGTCCACCT TTCAGTGAAG NGATAGTTAA GCCAATTCCN 360
N 361

SEQ ID NO:7579

SEQUENCE LENGTH:323

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08825

SEQUENCE DESCRIPTION:

GATCCAATTC GTGCTGTGG ATGCTGCAAG GACTGGCTCA TTGGAGCCAA ACCATGTGGC 60
GGAAACTCCT GAAATTGGTG GAAAAAGTGG AATATGGCAG ATTGGGTAGG TAGGAGAACA 120
ATTTTGAGA TTTTTTTCT TATGTTAAAG TGTCTGCATT TTATTTGCTG TACCCTGCCT 180
ACTCTGTTTT TNAGGATTTT TTGACTTCTT CGAAAAGCAC TGAATAATCT CTTNCCGGG 240
TCTAGATTTT TTGATGAGTA CTGTGTAAAA TTGTCAATAT TCAATGGATT ATTTAATAAT 300
ANNTTAAGAN TTCACTCAT AAN 323

SEQ ID NO:7580

SEQUENCE LENGTH:183

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08826

SEQUENCE DESCRIPTION:

GATCCTAAGT TAAGACTCTC CAAAGCAAAC ANTGGGTTTA AATCATTAT CTGATGTAGA 60
TAAAGGTAG AGAACTTGT AGTGTCTCC ACATAATGGA AAATGTACAA ATGCCTAGTT 120
GTGTGCCCCA TCAATTTTGT ATATNTCCAT AATTTTNATT GTTGANAATT GCATTATNTT 180
TTN 183

SEQ ID NO:7581

SEQUENCE LENGTH:350

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08827

SEQUENCE DESCRIPTION:

5 GATCCACCTG CCTCGGCCTC CCAAAGTGCT GGGATTACAG GCAGGAGCCA CCGCGCCTGG 60
 GCCTTTTTTT AAGTTTTAAG NNCCNATAAA GNCAGTGAAG GGTGATGTGT GTGGATGAGC 120
 TAGGAAGACC TGAATATAGC TCTCTCTAAA TTAATCAAAT TAATCCTGAA GCCATTCTGC 180
 10 AATACTGTCT TTAATGTATA CTCACTTGTT ATAGAAGCCA GGGTTTTTNC CCCTAATTG 240
 TATCATTGCT ATATGTGTTA TTGTACCAA CTACACTGTT TTAATTGCTG TAAATTTTAA 300
 TATGTCTTAG TATCTGGGTG TGGGAATCTT GANAGCATGG AGTTTGTGTN 350

SEQ ID NO:7582

SEQUENCE LENGTH:348

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08828

SEQUENCE DESCRIPTION:

20 GATCCTTGGG AGAGCTATCA CGGGAATCCA GGCCTTCACG GCCAGCAAGT GAGCCGCTCC 60
 ATCAGGGGCC CGAAACTNTC AAGCCCCCTT NTGGAGAGNT GCCTGGCTGG ACCGTAGAGC 120
 GCTGTGCTCT GAGCTTAGAA AGGGAGGTGG CGGATGGAGT GGGAAAGTGA AGACACTGAT 180
 TTTNAAATAT CAAAATTTCC CTTCTGAAGT CGTTCAGATG TTTTCTTAA AAAGAAGATG 240
 25 GAATTCCTCG TAGAGCGTCT CANTCCACTT TTAACCATGG NTGAGAGCAG ACTCCATTTA 300
 CCNTGAAATA GCAGCTTCTT TTGAGGGGAG AGTGACATGG AAGCAACN 348

SEQ ID NO:7583

SEQUENCE LENGTH:258

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08829

SEQUENCE DESCRIPTION:

35 GATCTGCAGG TTTGGGCATA TGCTTTCATC ATTAAATTAT CTGATAAAGT TACAAGTCAC 60
 AAAGGAGAAT GAGAACTTAA TGATTCTATT GGATTTAATA TATTAGCAAG AAANCATACT 120
 ATTTNCATAT GTNTAGCTTA GTAAGGCATT ANCATAAGTN CAANACCTAT GANACAGATG 180
 CNTATTTCTT CAACATACTG TGTCAGGTAT ACTGTTTTAT ANTTNGGTTG TTTTAGCCTT 240
 40 ATTGCACACC NNCTCCCN 258

SEQ ID NO:7584

SEQUENCE LENGTH:308

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08830

SEQUENCE DESCRIPTION:

50 GATCCATTC ATTACAAGTA AAATATTACA AAATATTTAC AGGAAAATAT TAAAAATAAC 60
 TCAACACAAA AAGGCAAGAT GAAATAAACT GTTTTTTTT CTCCAGAAAT CTCTACTCCA 120
 GTGCCACAG CACACAAGAG TCAAAACAAA TAAGCAACTA AGNTCCTTAC GAAAAAGGNA 180

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CAGNTTGTTC CTAAACCAGA AGAGGAGGTT GCCCAGAAGA AAAAGATATC CCGGAGGAAC 240
CTGAGGANCC NAAACTTTTT GCCCGGGGG TAATTCNGNC TTTNNATTAA TTTNTTTAN 300
NGGGNNNN 308

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SEQ ID NO:7585
SEQUENCE LENGTH:36
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08831
SEQUENCE DESCRIPTION:
GATCTCTTAT CATAATAAAG AATCTTTGTC ATCAAA 36

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SEQ ID NO:7586
SEQUENCE LENGTH:227
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08832
SEQUENCE DESCRIPTION:
GATCTAAGGA GGCCAGTGAA TTTCAAACAG GATTAAAAAG AAAAAAACA GAGTTAGGTA 60
TCAAATTAAG AATACTGAAA GCAAAGATAT AANTAGAACT TAAAAAGCAG CCAGAAAAAC 120
AAACATATTA CATATAGGGC AGCAACANTA AGANTAACCG CTAACTTTGT ATTAANNGTA 180
ATATAATTCA CAATACANTG TAACANCANT TTTNNGTGCT AACNGGN 227

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SEQ ID NO:7587
SEQUENCE LENGTH:215
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08833
SEQUENCE DESCRIPTION:
GATCTATTGA GAATGGAATT GTTTTCTTAA TTTTATTTTC AAATTGTTTG TTGCTAGCAT 60
ATAGAAATAC AAGTGATTTT NTATATTGCT CTTGTATCCT GTGACTTTGC TGAGCTTATT 120
TTAGTAGTTT TTTTCACTG AATTCTTTAG GATTTTNTAC ATAAAAAATT CATATCATCT 180
GTGAATAAAG ACAGTTTAT TTCTNAATTT TTAAT 215

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SEQ ID NO:7588
SEQUENCE LENGTH:43
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08834
SEQUENCE DESCRIPTION:
GATCATATTT TTAATAAAG CATTTTTTGT AGAAAGTGCT AAA 43

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SEQ ID NO:7589
SEQUENCE LENGTH:334
SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear

CLONE:HUMGS08835

SEQUENCE DESCRIPTION:

5 GATCAGGATA ACCAGGATGA TAGCAGTGAC GATGGATTCC TCGCTGATGA CAACTGCAGT 60
 TCAGAAATAG GACAGTGGCA TNTAAAGCCT ACTATCTGTA AACAACTTG TATCCTACTT 120
 ATGGNCTCAC TCCGAGGCC TTCTCGGTCA AATGTTGTCA AAATTTTAAG AGAGTATTTA 180
 GANGTGGAAT GGGAAAGTTAA AANAGGAAGC NNNAGANGTT TTTCCAAAGA GAAAAGAAAG 240
 10 CATAAGGNCA CTTACTCAAC AGANGCACCT TTAGGCGGNG GANCAGNACA TTGTGTCAAT 300
 AGTNTCTCNG GTTTGCCCTT TCTNTTACTT GTCN 334

SEQ ID NO:7590

SEQUENCE LENGTH:235

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08836

SEQUENCE DESCRIPTION:

20 GATCAAATTT AAAAATCAGT TTTAAAAGTG GTTCCCGACT TCTTTCCTTT GGAAGAATTT 60
 GGNCTNATGC TCATAAGCAG TTCATGAGTG ACAAGTGTAG CAAAAGCCAG CCATATATTT 120
 CNAGANTCTA TATCCTCAGG AAATGGTCTT TTTTTTCCT ATAANTCACC AACCAACTAT 180
 CTAANTGGNC ATTTGGGGGA NTTCCCTCCC AAATTTGATT TTNTNATTNG AAAAN 235

25 SEQ ID NO:7591

SEQUENCE LENGTH:172

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08837

30 SEQUENCE DESCRIPTION:

GATCCAGAGC ACAGATGGCA AGTTGTGTGG ATGATACTGA ATATNTTAT TTTCTAAAG 60
 ATAAATNTCA CGACACGACA TTTCTCAGTT TTAATTTAGA TGTTTATNAC CATGTGTAA 120
 35 CAGAATCTTA AAACCAAGG NATTTCTTCA GTAAACTAGA CTTTGATTCA AA 172

SEQ ID NO:7592

SEQUENCE LENGTH:335

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

40 CLONE:HUMGS08838

SEQUENCE DESCRIPTION:

45 GATCAAGAGG AAGCATGACT TGCACAAGAT GGCAGAGGCC AACCGTGCCC TGGCCCACTA 60
 CCGCTGGTGG TAGAGTCTCC AGGAGGAGCC CAGGGCCCTC TGCCGCAAGA AACAGTGTGA 120
 GCTACTGCCA CGCTGAAAAC TACCTGTGGG TTAAGGATGT AGTTCCTTTG TAAGGGTGGG 180
 CAGGCCTCGT AAGAAAGATG TAGCAGCATA TTCACTATCC GTTAATCCTT CTTTCTTTGA 240
 GGCTGGAAT TGCTCTCTCT GCCCCTATTT CCTTGTAAG AGGGAGCACA TTGACTTGGG 300
 AATTCCTCC AGGAAACTCA GGGCTGTTTT CTCTN 335

50 SEQ ID NO:7593

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SEQUENCE LENGTH:333

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08839

SEQUENCE DESCRIPTION:

GATCTGGGAC TTCTTTAGTA TCGAGTCTCC TTTGCACTCT TAAAAATTGT TGAGGACCCC 60
 AGAGAGCTTT TGTTTTATG GGTGTATCT ATCAATATT ATCATGAG AAATNATTTA 120
 TTTATTTTAA AATAACTTTT TTATTGAGAA AGATAGCAGT GTTTTTTTT AATCTTGCAA 180
 ATTGTTTAAT GTTTGATTTA ATGGAAGACA GCCAGATTGT CCTATCAGCA TTCAAACGTC 240
 TGCAGTAAGT TGTTTGAAT AATGTATATG AGGAAAACCT GACCTCACTG AGATTTTAAT 300
 TGGAAAATGG AGGAGTATTT TNCCAGCCTT TNN 333

SEQ ID NO:7594

SEQUENCE LENGTH:220

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08840

SEQUENCE DESCRIPTION:

GATCTCCTCC ATACGGAAC TTCTCATCTA CGTGGCCCTC CTGCGAGTCA CTCCATTAT 60
 CTTAAAGAAA TTGGACAGCA TATGAAGACA GGACATCACA TATGAATGCA CGATATGAAG 120
 AGCCTGGTTA CAGTTTCGAC TCCTCTCTGC AAGTGAATAG GCCCAGAAAG GTGTAAGAGA 180
 CTCTTTGAAT GGACATAAAA TTCTGCTTGT TAAGAACAAA 220

SEQ ID NO:7595

SEQUENCE LENGTH:326

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08841

SEQUENCE DESCRIPTION:

GATCTGTGCT GGCCACGTGC CCGGNGTCTC AGCTCTGAAC CTGCTGTCCC TGCTGAGAAG 60
 CTCTGAGGGC CCTCCCTGG AGGACCTGTG AGGGTGGCTG GCCCTGGGC TGCCCTTCT 120
 NATGGCTTCG TGCTGACTCC ATAAACATTC TCTGTTGAGG ATGTCCAGTC AGGGCTTGAC 180
 AGGCCAGGN TCAGCCGCC GTGGCTGGA AGGTTCCCTG CAGTGCCAGT GCTGCAGCAG 240
 GGAGAGCTGG GCAGAAGCAG CGAGGGGGCC CAGCTGGCGA GACTGTAGCC CCGTCCCACT 300
 CCCACACTCA CTCTGTTAG AGCCTN 326

SEQ ID NO:7596

SEQUENCE LENGTH:327

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08842

SEQUENCE DESCRIPTION:

GATCAGATGT TGAACGTGC TATGCTGTAG CGTGTCTGGA AACAAAGTAC ACAACCTGG 60
 CTACGGTGAT GAGTTAGCTT CTGCTTACTA CCTGTNACAA CCCAAGTGGG TGACACTAGT 120
 GAACCTTCTC CAGTCTGCAG GCTGGCATAG AAGGCTCTTA GATTATATTG GGCAGCTTGC 180

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AATCTGCCGA AGCAGTGACT TGCATTTCCA CACTTGGCTT GAGCACTCAA CCCAGAAGGC 240
GAAGATAGCT TTTGGTTGTA GCGGGCTTCC TGTATGGGAT ATCCCTCGGT AAGGGTAAAG 300
GAGCAGAGGC AAAGGAGAAA AGCAGTN 327

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SEQ ID NO:7597

SEQUENCE LENGTH:278

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS08843

SEQUENCE DESCRIPTION:

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GATCTTTCCT CCCTCCCTG CATGAGGCAG AGGCAAGCTG CCTGCCAACC CCCTCCCTCA 60
AGGAATGGCC TTGCCAGGA ATGCCACCA CACATACCCT CTNCTTTTTT NNTAGTCAAA 120
CTCTTGTTA TTCCTGGNT TGCNTCCCTC CTTCTCCCC TCTCAACCTT TACTTCTGAT 180
TTNNATTCA TGGAAATTGG GATTGANGTT AAATAACAAC AGTGCCGCCA ACACCAAGTN 240
TTGCAGGAAA AAAATACAAA GAAATTTANC ANANAANN 278

SEQ ID NO:7598

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SEQUENCE LENGTH:202

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08844

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SEQUENCE DESCRIPTION:

GATCTTCATT ACCGTTNCAT GATTGGAAAT ANTTAAAACA TTGTACAGTT TTAGTATAGA 60
GAAATNTAAT GGNTTTTGT AACCAGTTTC TGTCTGCATG TAATTGGAT TTCTCAAATA 120
CATTATTAG TAATTNATCA GTACATTAG TTTTATTNN GTCCATCTCC TTATCTATAA 180
AANGGGGATA TNCTTAGGAT NN 202

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SEQ ID NO:7599

SEQUENCE LENGTH:47

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS08845

SEQUENCE DESCRIPTION:

GATCCATAAT ATAGCATCAC ATCTCAATAA ATTTATTGG AAGCAAA 47

SEQ ID NO:7600

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SEQUENCE LENGTH:327

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

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CLONE:HUMGS08846

SEQUENCE DESCRIPTION:

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GATCTGCCCC CTTGGCCTC CCAAAGTGCT GGGATTACAG GCATGAGCCA CTGTGCCTGG 60
CCCCCTCCTG TAAATTTTN AAATGGAGAA TTGGGTGCNA GATGTGGTTT CCAGCCTGGT 120
GCCTGGGGTG CTGAGCTANN NGAGTGGTGC AGTCCAGGAC ACCTTTGCTT TATCTCACTT 180
ACACGGTCAC CTGGAGCCGG CTCAAGTGGC TAAAGCATCC TGGGGCCCAG AGCCAGGTGA 240

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EP 0 679 716 A1

TAGGTCCCTN TGGCCAACTG GACAGTTGAG GCCTGTGGTT ACCCGAAGCC CAGCTTGGGG 300
CCCTGGTCCA GCCTNGCCTC CCAGGAN 327

5 SEQ ID NO:7601
SEQUENCE LENGTH:326
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08848
10 SEQUENCE DESCRIPTION:
GATCTAGATG CTGGTATTGA GGTGGGAGAC AAGTACTGCC ACCNGAAACA ACAGTCTTGG 60
TAAATTTAGC CGACGAGGGT AAACACATCC TAACAGGGAA GGTAACTGT ACGTCCATCA 120
GTACCACTAG AGGGCATCNC NGGTTTATAG TTCAATACAG TGAATATATC AGANTAATGG 180
15 CCTTTAGTTT TCCTGAAAGA TTAANTTAGG CTTGCTAACT TGTTTAATGN GATANTCAAA 240
CATATGATGT AATTTTAAAG GGTTTACATT TTTANAANTT TAATGGTTGC TACATAAAAN 300
GGGNTTCAGT TAACTNATTT TGC GTN 326

20 SEQ ID NO:7602
SEQUENCE LENGTH:310
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08849
25 SEQUENCE DESCRIPTION:
GATCTCAGCA GGGAAACCATG GAAGCACCCA CCCCCTTGCA TTTTGGCTTA CCTGTAGCGG 60
AATGCAACAG AGAATTTTAT ATGCTAAGAT TTGTGGTTCC GTGGGAGAAT ATTTCAAACA 120
GGTGGAAACC ATCAAATAA AAGAGAACCA GAAATCATT AAAGGTCACG TGAGGAGCTT 180
CTGTNTTGTG CAACTTAAGC CTTACCAGT CTCCTATGCC CAGGTGCCCA GCACCCCAT 240
30 CATCTGCATA TTCACCATCC TCAGGTCAGA TTCTATGATA CTGNNAATAA AGGCATTCTG 300
GAAAANTAAA 310

35 SEQ ID NO:7603
SEQUENCE LENGTH:287
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08850
40 SEQUENCE DESCRIPTION:
GATCCGGTCA GCAGCCCCTG TGGCTAGAGG AACACCAGCA CAAACGACAG CCTCAAGTCT 60
CCTTCGAGCT TTATATCCAT TTGGGGATGA AGTCTACTTT NACAGCTAGC AAGGCGACAT 120
GCAACTGTTG TTGAATGATG ACAGCAATTC AGGAAAGACT TAAATATGAA AGCAAATTGA 180
NCACATCGGG TGTTTGTNAT CAGANNAGNG NTGNGATGTG ATAAGACTTG TTTATTGACT 240
45 AGCCAATATG TCATTACCT TCNGGTTTAT NTTGTGNANC CCCANN 287

50 SEQ ID NO:7604
SEQUENCE LENGTH:66
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

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CLONE:HUMGS08851

SEQUENCE DESCRIPTION:

GATCGAGTTT TGGTTCGGGT TAACTGTGTG CCTACTGAAC CTGGCAAATA AACATCACCC 60
 TGCAAA 66

SEQ ID NO:7605

SEQUENCE LENGTH:339

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08852

SEQUENCE DESCRIPTION:

GATCTGGAAT GTGAAGCGTT ATAGAAGATA ACTGGCCTCA TTTCTTCAAA ATATCAAGTG 60
 TTGGGAAAGA AAAAAGGAAG TGAATGGGT AACTCTTCTT GATTAAGT TATGTAATAA 120
 CCAAATGCAA TGTGAAATAT TTTACTGGAC TCTATTTTGA AAAACCATCT GTAAAAGACT 180
 GAGGTGGGGG TGGGAGGCCA GCACGGTGGT GAGGCAGTTG AGAAAAATTG ANTGTGGATT 240
 AGATTTTGAN TGATATTGGA TAATTATTGG TAATTTTATG AGCTGTGAGA AGGGTGTGT 300
 AGTTTATAAA AGACTGTCTT AATTGCATA CTTAAGNTN 339

SEQ ID NO:7606

SEQUENCE LENGTH:337

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08853

SEQUENCE DESCRIPTION:

GATCCTTTGT GAGCAAGTTC TATTTGTTCA TTGCTTGCCA GAGATGAACA CAGAAATGTT 60
 TGTTCATTT TACAAGAACT ATCCTGAGTT TCTGTGGATG GAAACATTAC ATGTAATGCA 120
 GATATAGTGA ACACGTGAAA GATTTATTA AGANTTATAT TTGTGTATAC TTTATAAATT 180
 AGTCCCTCAT TAGATTTTTT TTTCTTAAG CATAAGACTG ANCTTAAATG TGTTAATTTT 240
 AGTAGAATCA GGCACGTCTC GCAGAAGGAN CACAGATTGT NGAGATTAAC ATAAATNGTT 300
 CTTGTTCTAA TATATATNTN TNNCCATTTT TGTCGAN 337

SEQ ID NO:7607

SEQUENCE LENGTH:203

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08854

SEQUENCE DESCRIPTION:

GATCCGTGGA TTGAGGGTGC CTTTCCATTT ATTTTGGTCT TCTTACTTT CTTTCAACCA 60
 AGTTTTGTAG TTTTCAGAGT ATAAATTTTA TACTTGTTT GTTCAGCCTA TTAAGTTTT 120
 ATTTTGGTG CTATTGTAAA TNAATCTTC TTAATTTCAA TTTCAGATTA TTCCTTAAA 180
 TATACAGAAA TACAGCTGAT AAA 203

SEQ ID NO:7608

SEQUENCE LENGTH:207

SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear
 CLONE:HUMGS08855
 SEQUENCE DESCRIPTION:
 5 GATCAAACT TTTATAATA CAAAGACATT ATTATTTGNT TTTTCACTG TCCCCTCCTG 60
 AATATACAAC GGAGCATTCC AGATGCTAGA GTGACAGCCT CACTCAGACT CAGGGGATGC 120
 ATGCTTG CNT GTACAGTACT CGTATGTTTT AAATTGTTT TAACTCCTAA TATGTAAGTA 180
 TCAATAAATA TAATCACCTT AAGTAAA 207

10 SEQ ID NO:7609
 SEQUENCE LENGTH:249
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 15 CLONE:HUMGS08856
 SEQUENCE DESCRIPTION:
 GATCTTCGTG GTGGAAAGCT AAATTTTAAA ACCACCCCAA TGGATGCAGA CAGTGATGTT 60
 GCATTGGACA TTCTAATTAC AAATGTAGTC TGTGTTTNA GAACAAGATG TCATTTAANC 120
 TTAAGGAAGA TTGCTTTGGA AGGNGCAAAT GTAATTNATA ANCGTGATGT TGGAAAAGTA 180
 20 TTANTGAGGC TTAGAAAACC TAGANTTACA GCTACANTTN GGTCTCAGG AAANNTTATT 240
 TGCNCTGGN 249

25 SEQ ID NO:7610
 SEQUENCE LENGTH:319
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08857
 SEQUENCE DESCRIPTION:
 30 GATCTGTAGT ATTTAATGT GCATCTACTT TAAATGAGTC ATCTTGGGGT TTTTATAATT 60
 CCCTTATGTT CTCGCCCTC TACACTTGAA ATAACAAAAT GCCTTAATTT TATGGATTAG 120
 NTCTCTTATA GGAGACAGGC AGCTATATGN AGCAANCCCA GTAAAGTTAT TTTTCAACTN 180
 TCANAGTTGT AAAATATTTT ATAACAGTTT ACANCAACAG CTGNAGANCA ACATGCCACA 240
 35 TTTNTTTTGC AGCATTTTCA AATANTTTGT TTTGTGGTGT NAGCACAGGN TAAANNTGGG 300
 GNGCGTCGAT GTGAGGCGN 319

40 SEQ ID NO:7611
 SEQUENCE LENGTH:208
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08858
 SEQUENCE DESCRIPTION:
 45 GATCTACAAA AAATTCCTGG AGCCATATAT ATACCCTCTG GTTCCCCCT TCGTTAGTCG 60
 TATATGGCCT ANGAAAGCAA TACAAGANTC CAATGATACA AACAANGGCA ANGTAACCTT 120
 TAAGGGTGCA GACATGAATG GTTTACCAAC AAAAGGNCCA ACAGAAATCT GTGATAANNC 180
 GNAAGACTAA NGAAATTTTC CNAAGGN 208

50 SEQ ID NO:7612

55

SEQUENCE LENGTH:321

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08859

SEQUENCE DESCRIPTION:

GATCTTCCCA CCTTCAGCCT TCCAAGTAGC TGGGACTACA GATGCACACC TCCAAACCTG 60
GGTAGTTTTT NAAGTTTTTT TGTAGAGGTG GTCTAGCCAT GTTGCTAGG CTCCCGAACT 120
CCTGAGCTCA AGCAATCCTG CTTCAGCCTC CCAAAGTACT GGGATTACAG GCATCTNCTG 180
TAGTATATAG GTCATGAGGG ATATGGGATG TGGTACTTAT GAGACAGAAA TGCTTACAGG 240
ATGTTTTTNT GTAACCATCC TGGTCANCTT AGCAGAAATG CTGCGCTGGG TATAATAAAG 300
CTTTTCTACT NCTAGTCTAA A 321

SEQ ID NO:7613

SEQUENCE LENGTH:136

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08860

SEQUENCE DESCRIPTION:

GATCCTTCTT AGGGGATGGG GGAAGCCCTG GCTGCAGGCA GCCTTCCAGG CAATATGNNG 60
ATAGGAGGCC CACGGGCCTG GCAGTGAGAG GTGTGGCCCC ACACCGATTG ATGATATTAA 120
AATCTCAACT CCCAAA 136

SEQ ID NO:7614

SEQUENCE LENGTH:47

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08861

SEQUENCE DESCRIPTION:

GATCCCGTCT CTACAAAAAA TAAAAAATAA TTAGTCGTGG TGCCAAA 47

SEQ ID NO:7615

SEQUENCE LENGTH:36

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08862

SEQUENCE DESCRIPTION:

GATCACTTTT TCAATATTAA ATNTTATTTA CATAAA 36

SEQ ID NO:7616

SEQUENCE LENGTH:260

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08863

SEQUENCE DESCRIPTION:

GATCATCATG AAATNATAAG AGGGCTTAAG AATTTGTCCA TTTGCATTG GAAAAGAATG 60

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ACCAGCAAAA GTTTACTAA TACCTCTCCC TTTGGGGATT TAATGTCTGG TGCTGCCGCC 120
 TGAGTTTCAA GAATTAAGC TGCAAGAGGA CTCCAGGAGC AAAAGAAACA CAATATAGAG 180
 GGTGAGATT GTTAGCAATT TCATTCAAAA TGCCAAGTGG AGAAGTCTGT TTTTAAATAC 240
 ATTTTGTGT TATTTTAAAA 260

SEQ ID NO:7617

SEQUENCE LENGTH:102

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08864

SEQUENCE DESCRIPTION:

GATCAACTTT AGTCACCAAC CCAAATGGAG GATTINTGGC TTGTGGGNCC TTATATGCCT 60
 ATAGNTGTGG ACATTGTCAT TACACAAGT GANTCTTNC TN 102

SEQ ID NO:7618

SEQUENCE LENGTH:228

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08865

SEQUENCE DESCRIPTION:

GATCAAGGGG CCTCTCAGAA CCATGTTCCC CAGCCAGGTG AGGACCATT TAACTGGGAC 60
 CCAGGNCAAA ACCATGTGGG TGCACAAAGC CAGGCACTGC CAAGTGGAAC ATGAGGTTAT 120
 TTCCAAATCA TGGGAGCCAC CAGCAGGGAG AGGGCAGTAT GGAAATCCC CTGGAGCCGG 180
 TCAACTNTT GTCATGGCT AGTGAAATAA AGTTGTTGA GTACTAAA 228

SEQ ID NO:7619

SEQUENCE LENGTH:113

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08866

SEQUENCE DESCRIPTION:

GATCTCTTAC TCCCCAGTT TGAATGGTAA ATTTGAATGG TAAATCCCA TGAACATATA 60
 TGGAATATC TTTATCCTAC TTTNTCCAAT AAAGGCTGTT CTTAGCTTTT AAA 113

SEQ ID NO:7620

SEQUENCE LENGTH:279

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08867

SEQUENCE DESCRIPTION:

GATCACCTGN CAAATGTTTG AGGACGGAGC TGTGCAGTCA CATTATTGGG GATTCCACAG 60
 CTGGTGCTGC AGGCCTTGCG CCTCCAACCA GGACTTTNTT CTTAATGCTC TCGACACTTA 120
 GCTAAACACG ACTATATCCC GGCCACGAG GCGCCAGCGC CGTTAGTCTC CAGCTGACTC 180
 TGTGGGTTGG TCTTAAAGCA AATTCTGTTT TGTGGACTGC CTGGCAATTT TTNAGCTAAC 240
 TGTAATGATA AAAAGGGAGT NTTAATCTAT TCTGAATCN 279

SEQ ID NO:7621

SEQUENCE LENGTH:198

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08868

SEQUENCE DESCRIPTION:

GATCAAGTTG TGGTGGATAA CGTGTTCCTCA AATTGCATCT TGTGCTGAA ACTTCCTGGA 60
 CTTGAGAAGT TACTTCATCA TGTGACAGAG GAAAAAGGTA ATCCAGAAAT AGACAACAAG 120
 AAATATTACA AGTNCAGCAA AGNGAAGACA TTAAAGTGGC TGGNAANNNN GGTTAATCAA 180
 NCTGTGGCAG CATTAAANN 198

SEQ ID NO:7622

SEQUENCE LENGTH:184

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08869

SEQUENCE DESCRIPTION:

GATCCAGAAA GTAGCAATAT AGGACTTTAA GGGGTATGTA TTAGTGTAAT TAATATATGT 60
 GCAGTCTAGG CTAATCATNT TAATTAAAAA CAAATAAGCA TACTTTTTTN CTTTAAAAAT 120
 ATGCCCTCAA AATGGTGGGG GATAAANTGT AAGATATTCT TTAGCTGNNN TTATTNNCC 180
 GNCN 184

SEQ ID NO:7623

SEQUENCE LENGTH:212

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08870

SEQUENCE DESCRIPTION:

GATCCTAAGT CTCCTACAAA AGCTTTGAAT ACTGTGAAAA TTTTTACAT TCCATTTCAT 60
 TTGTGTTGTT TTTTAACTG CATTTTACCA GATGTTTGN TGNATCGCT TATGTTAATA 120
 GTAATCCCG TACGTGTTCA TTTTATTTTC ATGCTTTTTC AGCCATGTAT CAATATTCAC 180
 TTGACTAAAA TCACTCAATT AATCAATGNA AA 212

SEQ ID NO:7624

SEQUENCE LENGTH:373

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08871

SEQUENCE DESCRIPTION:

GATCGCAGAC CGCGCTGCCC ACGACGAGTC CCCGGGGAAC AACGTGGTTG GACATCAGCG 60
 TGCCGCCAC CACGGACGGA CAGAAGTCTC TTTAAGAAAA TAGTTTAAAC AATNGNTAA 120
 AAAATTTCC GTCTTATTTT ATTTCTGTAA CAGTTGATAT CTGGCTGTCC TTTTATAAT 180
 GCAGAGTGAG AACTTTCCCT ACCGTGTTTG ATAAATGTNG TCCAGGTTCT ATTGCCAAGA 240
 ATGTGTTGTC CAAAATGCCG TTAGTTTTT AAAGATGGAA CTCCACCCTT TTGCTTGTT 300

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TTANGTATGT ATGGAATGTT TATGGATAGG GACATAGTAG TAGCGGTGGT CAGACCATGG 360
GAANTGGGTG GNN 373

5 SEQ ID NO:7625
SEQUENCE LENGTH:74
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
10 CLONE:HUMGS08872
SEQUENCE DESCRIPTION:
GATCCTACAA GCATGTCTGC TGTAACCTA TGTATGTTTT CTGTAAAATC ACATACCTAT 60
AAAATAAAAA GAAA 74

15 SEQ ID NO:7626
SEQUENCE LENGTH:53
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
20 CLONE:HUMGS08873
SEQUENCE DESCRIPTION:
GATCGTGAAC ACTGCATTCC AGCCTGGGTG ACAGAGCCNG ACCCTGCCTC AAA 53

25 SEQ ID NO:7627
SEQUENCE LENGTH:379
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
30 CLONE:HUMGS08874
SEQUENCE DESCRIPTION:
GATCTACCCA CCTTGGCCTC CCAAAGTGCT GGGATTACAG GCGTGAGCAC CGCGCCTGGC 60
CCTCTGCAGT TGTTTAATAA GGCACAGAAT ACCTGTAGCA TAGGTCAGCC TTACGATGTC 120
CATGAATTAC ATATTCAGAC GTTTTAGAGC CTGATACATT TTGGAANCGA AAAACAACCT 180
CTACACCTAT TCTACAGTCC GCATTAAAA CAATAAATC CTCTATTAAT AACGTAAAGC 240
35 CGGGTTTGCT TCGGTGCCAC AGGGGGTATA TCCAGGAAGG TTATTATGAA GCTGTCAAAT 300
CAAGATGATG GNAATAAGGC AGTTTGAACG GACAGTCTTC CCACAGTCAG GCCATTTTTG 360
CTGATTGGT TTAGGATTN 379

40 SEQ ID NO:7628
SEQUENCE LENGTH:212
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
45 CLONE:HUMGS08875
SEQUENCE DESCRIPTION:
GATCGGGCGC TGTGCAGTGT GGTGAGCATG GTGAAGAAAG TCATTTCTC GGTGGGCAGT 60
ATTCCTCTTT ATCTCTCATT AACTGGAAGG TGTTATTTCT GCTGTATCAT CCGTGCTCAA 120
CGTTTTAGTC TGTCAGGCTC ACCTCTCTC TGGAAAGAAT TTGCTTAAT TGACATTCCA 180
50 TGTGCCGCTA ATAAATATA TTTTGAAGA AA 212

55

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SEQ ID NO:7629
 SEQUENCE LENGTH:350
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08876
 SEQUENCE DESCRIPTION:
 GATCAGAANT AATTACCATT CCCNGTGTTC TGCTGTAGGA CCTTCAGGTC TATGTTCTAA 60
 GTGGGGNTTA TGAAGCTGGT AATAGAAAAT AATGGAGAGC AGTTAAAGAG TTAATATACA 120
 TTATTAATAT GNGTGTCTC TACAGGCACA CAAAGCCTGT AGACTCAACA AATTTACTCC 180
 TGAAGTTTTT CAAATTTGCA AAATCTGCAA TTTNTGTGCC ACATAAAGCT NTCCAGAAAT 240
 TGAAAANCNG TAAANCACCG GGTCTCANTT TTTTCCTGCA TTTCACTGAT ACCTTAANTT 300
 ACATAGNTTA NCTTCTTTAN AGCACTACCT TTTNGCTGT TGNTATTAAN 350

SEQ ID NO:7630
 SEQUENCE LENGTH:76
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08877
 SEQUENCE DESCRIPTION:
 GATCTCACAA CTGCACTCCA GCCTGGTGAC AGAGCAAGAC TCCATCAAAA ATAAACAAAT 60
 AAAACAAACA AACAAA 76

SEQ ID NO:7631
 SEQUENCE LENGTH:185
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08878
 SEQUENCE DESCRIPTION:
 GATCAAAGTC TGCTTCATTG TCTTGTCCC CATTTTAATG GCAATGTTAG GTATAATNTT 60
 TGCTTTTATT AAGTATAATN TTTGCTTTTG TTGGTAGAGT TTTACGATTT TACATCAGAA 120
 GTACCTGTTT AACTTAATTG CCACGTTTAA GCATCAATTA AAATATTTTC ATTGAACTCA 180
 TGAAA 185

SEQ ID NO:7632
 SEQUENCE LENGTH:149
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08879
 SEQUENCE DESCRIPTION:
 GATCTTTTAG GAATTAACT TGCAATNAA ATGAAATATG TTGGGACTTT GGCATAATTT 60
 GAATATAGCA TTGTGTGAGT TGTGATTGTN TCTTCCTAAT TGTGCTGTAA TAACCTGTGT 120
 ATGAGAATAA AATGATTTC ACCATCAAA 149

SEQ ID NO:7633
 SEQUENCE LENGTH:193

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08880

SEQUENCE DESCRIPTION:

GATCTCACTC CATGATTACT GTGTAAATA TTTTGCAC TTTGTGAAGT ATTTTAACT 60
 TTTTCTGTA CATAACTGTG TTCTCAGAGC TGAATGTTA TATCTTTTGC TGTGCAAAAG 120
 AAACANNNA AATGTTGTTT AGTTGTATAT ACAGAAATGT GTATAAAACA TTTTGTATT 180
 TTTNAAAAGT AAA 193

SEQ ID NO:7634

SEQUENCE LENGTH:148

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08881

SEQUENCE DESCRIPTION:

GATCAAGAAT TTTGTAGAGT GGACAGTCAT TACATATGTT ATAAC TTATC CTTTAAAAAC 60
 TATTTTAAAC TTTATCCTTT CAGCTTTACT TAGTGCGATG TTTTAGAAGC AGTCTTCAA 120
 GAATAAAACA CTAACCATGC ATGTGAAA 148

SEQ ID NO:7635

SEQUENCE LENGTH:376

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08882

SEQUENCE DESCRIPTION:

GATCCATTTC TGTGTCCTNT AGCCTAGTAT GTCTGAACTT CCATTCTTGT TATATATTTA 60
 AACTTTCCTT CTATATTATA GGNTTNGTGG CNCCACGGT CAGGTGTAGA GGAAGCTGCC 120
 CCTTGCAGAA CTGTACTGTA ATATTTTCT TTTATAAATA TTTTACAGG ACTGATTGTA 180
 CACAGGGCTT GTAATAAAAT TTTAACACTG TGCTGTGAAA CAACTATGGG GAATCTCCAT 240
 TGAAGGCTAC TTCTATGGCA CCTGAAAGTG GAGTGTATA GCTATGACTT TCTATTTCTT 300
 GTTTCCTAAG TAAATTAAC CTAATTTTCA CCCTTTCATT CTGTTTCAGC CTCCTGTNTA 360
 AGGAAGTACC GTTTGN 376

SEQ ID NO:7636

SEQUENCE LENGTH:279

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08883

SEQUENCE DESCRIPTION:

GATCCCATTC ATTGTCCCTT TTGGGGTATT TCCAATACTT GAATGGCAGA TTGGAGTTTT 60
 TCAGAGTATG TGTTTCATCT GCTAGTCTTT CTCTCCTTCA TAGCTTTTCT TTTCTGGAC 120
 TTGCTCCTTT TGAGTTGCTT TTGCGTTTCT CATGCCTAGG CAAGTGTAAT AGAAATTATG 180
 TAGCTCCTTA TGTTGGCAAA GGAGCTCTAT ATAGTTTCAC TTTGTATACA AGTTAGGNCC 240
 AGCTGTTGTT ACATGTAATA TNNTGGTTCA GAACTTGAN 279

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SEQ ID NO:7637

SEQUENCE LENGTH:373

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08884

SEQUENCE DESCRIPTION:

GATCTCTGAT TGCATCTATG TGGATTCTTT TTGGAGGTTA TGTGCTAAA GAAAAAGACA 60
TAGTATACCC TGGAAATTGCT GTATTTTNC AGAATGCCTT CATCTTTTT GGAGGGCTGG 120
TTTTTAAGTT TGGCCGCACT GAAGACTTAT GGCAGTGAAC ACATCTGATT TCCCACAGCA 180
CAACAGCCCT GCATGGGTTT GTTTGTTTT TTAGTGCTCA CTCCCAACCT TTTGTAATGC 240
CATTTNCTAA ACTTATTCT GAGTGTAGTC TCAGCTTAAA GTTGTGTAAT ACTAAAATCA 300
CGAGAACACC TAAACANCAN CCAAAAATCT ATTGTGGTAT GCACTTGATT AACTTATAAN 360
ATGTTAGGTG GTN 373

SEQ ID NO:7638

SEQUENCE LENGTH:53

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08885

SEQUENCE DESCRIPTION:

GATCACACCA CTGGCACTCC AGCCTGGGCG ACAGAGTGAG ACTCCGTCTC AAA 53

SEQ ID NO:7639

SEQUENCE LENGTH:363

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08886

SEQUENCE DESCRIPTION:

GATCCGAACCT GGACTCACAT CCTGTATGGT GGATGGACTG TATATTGAGG GTTCCATTCT 60
TCGCGCAGTT TAGACATCTC TGTTTTGATT CTTTGTGTT GTTTTATTT TAAAAGGCAC 120
AAACTCTAGA TATTAGTTGA ATGTTGAGGC TTAACTTTT TCGGTGTCTT TCTACAACTG 180
TGTTCTGTGA CTCAATTGTG TCGTGTTAAT ATCAGTACAG ACTGTCTCCT CTACGTGACC 240
GTATAATGTT TTTCTCTTCT TGTAAGTCTCT ATGGCGTGTC TTTATGGTGT AATAAGGTTT 300
TCACGGGTTT AATCTTTTGT GTTTAGGGNN NNCACGGTTC AGACCAAATG GTATATAATT 360
TTN 363

SEQ ID NO:7640

SEQUENCE LENGTH:270

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08887

SEQUENCE DESCRIPTION:

GATCTGGTTC TGAGGAGGAC ACACCTGGCA TCGGATGACC TTTATAAATT ATCTATGAAA 60
ATGCCAAAAG CTCTCAAGCC AAAGAAGAAG AAAAAATTT CCCATGATAC TTTTGGTACA 120
ACTTATGGAA GGATTCATAT GCAGAAGCAA GACCTAAGCA AACTACAAAC CAGGAAAAATG 180

AAGGGGTTGA AGAAGCGACC TGCAGAAAGG ATAACAGANG ACCACGNGGA AAAAGTCAAA 240
AAGAATTAAA AAAAATTGAT GGAACCTAAA 270

SEQ ID NO:7641

SEQUENCE LENGTH:336

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08888

SEQUENCE DESCRIPTION:

GATCTCTGAA AAGACGTTAT CACCTTAAAG CTCAAATTCT TTGGGATGGT TTAACTTAA 60
GTCCATTAAAC AATTCAGGTT TCTAACGAGA CCCATCCTAA AATTCTGTTT CTAGATTTTA 120
AATGTCAAAGT TCCCAAGTTC CCCCTGCTGG TTCTAATATT AACAGAACTG CAGTCTTCTG 180
CTAGCCAATA GCATTACCT GATGGCAGCT AGTTATGCAA GCTTCAGGAG AATTTGAACA 240
ATAACAAGAA TAGGGTAAGC TGGGNTAGAA AGGCCACCTC TTCACTCTCT ATAGANTATA 300
GTAACCTTTA TGAACGGGG CCNTNTAGTT TGGGTN 336

SEQ ID NO:7642

SEQUENCE LENGTH:331

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08889

SEQUENCE DESCRIPTION:

GATCCATTTC AGATACTTGT GGCAGCAAAC AAAGCAGTTC ACCTCTACAA ACTGGGAAAA 60
ATGAAGACAA GAACTCTATC TACTGAAATN ATTTTCANCC TTCCCCAAA TAACAATATT 120
TCAGAGGCTT TGA AAAAATT TGGTATCTCA GCAAATGACA CTTCAATTCT AATTGTTTAC 180
ATTGAAGAGG GAGAAAAACA AATAANTCAA GANTACCTAA TATCTCAAGT AGAAGGTCAT 240
CAGGTTTCTC TGA AAAANTCT TCCTGAAATA ATGATTATTA CAGANGTCAA ANAGGTATAT 300
AANCTCTCTT CACAGGNGGN ANGATCGGA N 331

SEQ ID NO:7643

SEQUENCE LENGTH:327

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08890

SEQUENCE DESCRIPTION:

GATCCACTGT CCGGCAGAGG AAAAATGCCA GCTGTGGGAC AAGGAGTGCA GGCCGCACAA 60
CCTCGGCAGG CACCGGGGGG ATGTGGCGAT TCTACACAGA AGATTCACCT GGGCTCAAAG 120
TTGGCCCTGT TCCAGTATTG GTTATGAGTC TTCTGTTCAT CGCTTCTGTA TTTATGTTGC 180
ACATTTGGGG CAAGTACACT CGTTCGTAGA TTCAGTTACA TCCATCTGTC ATCTGAAGAA 240
GGAGGAAAAA ACCCAACATT TCTTGGACCA AAAGTATAGT GACTATCTGT TCATGAGAGA 300
AATTTTCTGT NAGCTTGCTG TTTTGAN 327

SEQ ID NO:7644

SEQUENCE LENGTH:287

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08891

SEQUENCE DESCRIPTION:

5 GATCAAGATG AAGTTCAGCT AGAAGTCATA CCACCCTCAG GAATCAGCTA AGTAATTATN 60
 ACTTGATTCT TTTAGCAAAT CAATGCACGT NATCCTACTT AATCCTTAAA TAAGTTTAGA 120
 TTTAACTAAC CCAAAGTCCA GGAGGATGTT CTTACAAAAN TAGCTATATC ANGGGCTGGC 180
 ACCTAGACAT TAANCTGTAA TTNGANAATA AGCAACATGT TGCATAACTN GTTGAATAA 240
 10 TTCCTGTGNC TGTTTAACAC TTGTCATAAN TTAGCAGNGT AANNNTN 287

SEQ ID NO:7645

SEQUENCE LENGTH:327

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS08892

SEQUENCE DESCRIPTION:

20 GATCTACCCA ATTAGAAATG CAACTTGAGA AACCCAAACC TGTAACCA GTGACGTTTT 60
 CCACAGGCAT CAAATGGGT CAACATATTT NACTGGCACC TATTCACAAG CTTGAAGAAG 120
 CTCTGTATGA ATACCAGCCA CTGCAGATAG AGACATATGG ACCACATGTN CCTGAGCTTG 180
 AGATGCTAGG AAGACTTGGG TATTTAANCC ATGTCAGAGC TGCCTNACCA CAGGACCTTG 240
 CTGGAGGCTA TACTTCTNCT CTTGCTTGTC ACAGNGCACT ACAGGATGCA TTCNGTGGGC 300
 25 TTTTCTGGCA GCCCAGTTAA CCATTTN 327

SEQ ID NO:7646

SEQUENCE LENGTH:329

SEQUENCE TYPE:nucleic acid

30 TOPOLOGY:linear

CLONE:HUMGS08893

SEQUENCE DESCRIPTION:

35 GATCTGGCTG CTCATGAAGA CAAAGTTCTG AGTGTAGACT GGACAGACAC AGGGCTACTT 60
 CTGAGTGGAG GAGCAGACAA TAAATTGTAT TCCTACAGAT ATTCACCTAC CACTTCCCAT 120
 GTTGGGGCAT GAAAGTNAAC AATAATTGA CTATAGAGAT TATTTCTGTA AATGAAATTG 180
 GTAGAGAACC ATGAAATTAC ATAGATGCAG ATGCAGAAAG CAGCCTTTTG AAGTTTATAT 240
 AATGTTTTCA CCCTTCATAA CAGCTAACGT ATCACTGGGG CTTATTTTGT ATTTTATAAT 300
 40 AAGNTAGGGT TGTGTTTTNT NAAATNCGN 329

SEQ ID NO:7647

SEQUENCE LENGTH:93

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS08894

SEQUENCE DESCRIPTION:

50 GATCTTCAAG TGAACATCTC TTGCCATCAC CTAGCTGCCT GCACCTGCCC TTCAGGGAGA 60
 TGGGGGTCAT TAAAGGAAAT CTGGGACAAC AAA 93

55 SEQ ID NO:7648

SEQUENCE LENGTH:283

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08895

SEQUENCE DESCRIPTION:

GATCTGCATG CATTGCTTGC ATTTTNTTGG TATCTGAATG TTGGTTCCTT GTTCCAGGAA 60
 TTCAACATTA NTTTCCAAAA GTATCATGGG ACTTGTGACA ATACANGTCA TGAATCTATG 120
 TATAAAATTT ATCGGCCTTT CTCATTTACC TGCTCTAGTA TTATTGTATT GTGTGTGCGT 180
 GCGTGTGTGA TGTCAGGCTG CCACGTAAAA CTTCAGAGGA AAATCTTAAA NGCAGGCCAT 240
 CCTTTTNGC ATGCTCTATT CTAAGTAGGA ATGTTCAATG TAN 283

SEQ ID NO:7649

SEQUENCE LENGTH:276

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08896

SEQUENCE DESCRIPTION:

GATCACCTGT AGGTCAATAG TTCGAGACCA GCCTGGCCAA CAAGGTGAAN CCCATCTNTA 60
 CTAAAAATAC AAAAAATTAG CCAGGTGTGG TGGTGTGCAC CTGTAGTCCC AGCTATTTGG 120
 GAGGCTGAGG TGGGAGAATC ACTTGAACCT GGGAGGCGGA GGTTCAGTG AGCTGAAATC 180
 GCGTACCACA CTCCAGCCTG GGTGACAGAG CGAGACTGTG TTTCAAAGAA AAAAAAACC 240
 AGGCAGCCTT TTGCTTGGTT GGAATCTGAT TTTCTN 276

SEQ ID NO:7650

SEQUENCE LENGTH:182

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08897

SEQUENCE DESCRIPTION:

GATCTAAATA TTCAGGTTTT AAGCCTGCTG CAAACTTTTA AAATATTATG ATAGNTTCTG 60
 TACTACATGT GGGAAACAAG CAAGAACTAA ATAATCAAAT GTTGTCAACC AAAAGTAATA 120
 GTTGGGTATT GGAGATTTT TAAAAATGTT TTTATGTTAT TNGCTATTG GAGTTAAATA 180
 AA 182

SEQ ID NO:7651

SEQUENCE LENGTH:93

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08898

SEQUENCE DESCRIPTION:

GATCTNAGAA AACGTTTAAT ATCAGATTN TTTATTTTNN CCAACACAAC TGAATCAGTT 60
 TTCTTAAATA AAAGTTTATT GTCTACTGTT AAA 93

SEQ ID NO:7652

SEQUENCE LENGTH:275

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08899

SEQUENCE DESCRIPTION:

5 GATCTAAAGT TAGTTGCCCTT TGCCTGTAAA ACATGTGATT TGCAAATTAT TATTTTNNTT 60
 TTTTAAACA AATGGAAGTA AATTGTTC ACGTAAATCT TAATTTCAA CCTTTCTGGA 120
 TACCTTAATT GTAACGTCA GTTTCACCTG GTCGGTATAT GGAAACACAT TGCTCTACCC 180
 10 TGCTACTTAG TTGNTTTAA AGTGAATTN CAGTGATGNG AAATTGTGA AANNTATATT 240
 GTATTTCTTT TGATGTTTCA AAAGGTTGCC TATGN 275

SEQ ID NO:7653

SEQUENCE LENGTH:279

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08900

SEQUENCE DESCRIPTION:

20 GATCTTTAGG TGTGAACTG GGAATATGCT CTGCAACACC CAGGATTAGG ATAGAGATGG 60
 ATTTCAATTT ATATGGGCTA GCATATTATT ATTAAAGACC ATTCAGGAG TGGGACTGTG 120
 AAAGGAGGTG CTCTGTTATC TGGTCCAAGA GCTCCTCTGG GAATTAATCC TGGCTGGTTC 180
 TGATGAGCTG GCAAGGNGCA GNGGATTGCA GTCTTTAAGT AGAAAATTNG AACCCCATCC 240
 ATATAACACG TGNACGTGCA TTAAATAGCT TGAATTGTN 279

25

SEQ ID NO:7654

SEQUENCE LENGTH:264

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

30

CLONE:HUMGS08901

SEQUENCE DESCRIPTION:

35 GATCAAGACC AGAAAGAAAT TATTGATACC AATGGAGCTG GAGATGCATT TTTGGAGGT 60
 TTTCTGTCTC AACTGGTCTC TGACAAGCCT CTGNCTGAAT GTNTCCGTGC TGGCCACTAT 120
 GCAGCAAGCA TCATAATTAG ACGGACTGGC TGCACCTTC CTGAGAAGCC AGACTTCCAC 180
 TGATGGAAGA GCTGAAAACA CAAGCCCAGG AGTGCAGACA CTGCCCTAAT TGCTTCCTGA 240
 GAATCCCAT ATTAATAAAG ANGN 264

40

SEQ ID NO:7655

SEQUENCE LENGTH:61

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08902

45

SEQUENCE DESCRIPTION:

GATCTTTTAG GAAAAAAAT AAATATTTT AACATTAAAG CAGTCACTTT GGTATCAA 60
 A 61

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SEQ ID NO:7656

SEQUENCE LENGTH:66

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08903

5 SEQUENCE DESCRIPTION:

GATCTGTTTG CTTAGCTGTC AACAAAAAGA AAACCTGAAG GAGCATTGG AAGTCAATTT 60
GAGGTN 66

10 SEQ ID NO:7657

SEQUENCE LENGTH:252

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08904

15 SEQUENCE DESCRIPTION:

GATCTNACTA AGCTTTCTTA GGAAGGGAAA GCATCTGGCA AGGAGTAAAA TGTCTGTTTC 60
CAACAATTGT CCCTGTTCCC ACTACTTTTT AAAAATGTCC TTAGTAAAAA GTGTATATGA 120
GGCAAGATTA TATTGAAAAA NTGAATATAA GAAAAAATA TTATGTTAGA GAGNAACGTA 180
TTCAGCATTG TTNTCAAAAT CACAAACTGT TAGGNGACTC TGACATCAGG TTTGTTCTCC 240
20 ATATGCAGCA AN 252

SEQ ID NO:7658

SEQUENCE LENGTH:153

25 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08905

SEQUENCE DESCRIPTION:

GATCTACATG GATGTTCTGT TCTCTGAACT GTCTGGATGA ACCGGTCAAC GGCACATCATC 60
30 ATACCTTAGT TTTTAAATCT GCATTGTGGT CATAATCTGT TATTTAATTA ATTTCTCGTA 120
TTTTAATAA AAACTTTGCC TATATATTTT AAA 153

SEQ ID NO:7659

35 SEQUENCE LENGTH:23

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08906

SEQUENCE DESCRIPTION:

40 GATCCCAAAA GTAGCAAGAG AAA 23

SEQ ID NO:7660

SEQUENCE LENGTH:280

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08908

SEQUENCE DESCRIPTION:

GATCAATTGC AGAATGATAC AGATAGTACA ATGACTTTTT TGTAATTG AATTAAAAGT 60
50 TTCCTCATAA AACTCAGTAC TATCTATTGG TAATGGATGC ATATATGTAT GTACATGTTT 120

55

EP 0 679 716 A1

TTNAAACGGA TTGGAAGGAT ACAGACCAAA CTCTTGATAG TGGTCACCTG TGAAGAGTGG 180
AGAAGGGGAAA ATNATGAGTG TGGGAGGTGG GATGGGTATT GGTAAANGGG GACTTCAGCT 240
TTTTATATAA ACATCCACTT CTCTTCAAA AAGNCTTCAN 280

5

SEQ ID NO:7661
SEQUENCE LENGTH:137
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

10

CLONE:HUMGS08909
SEQUENCE DESCRIPTION:
GATCATTTTA AAAAAGTAA TCTATATNAT NTTTAACTTC AGAAGGCATC ATTTATAAGA 60
CAGTATGGCA GTTAATTATA AAATNATTTT GATGAATTAT GATACAATCT ACATAATAAA 120
GAATNCTTTT GATTAAA 137

15

SEQ ID NO:7662
SEQUENCE LENGTH:305
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

20

CLONE:HUMGS08910
SEQUENCE DESCRIPTION:
GATCCTAAAA CTGTCTCTCA CATTATATAG TAGATGTTTG TTTATAATGT TTACAAAACA 60
TTTTGGTGAA TTCTCTCAAT GTTTTATAAA TGTACATTTT TTAAGTCCTT AAGCTGACTC 120
TTAGCCATCA TGTAGCTTAA GGAGTCTGAA ATCTGCCATT AAAACTGCAC CTTTAAGCCA 180
GGTGTGGTAG CATGTGCCTA TAGTCCCAGC TACTTGGGAG GTGGAGGTGG GAGGATTATA 240
AATAGAGACT TTCCTTAAGA CTTTAAAAAT GTATTGNAA ACTATTTTTT ATTAAATACT 300
TTGTN 305

30

SEQ ID NO:7663
SEQUENCE LENGTH:103
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

35

CLONE:HUMGS08912
SEQUENCE DESCRIPTION:
GATCCTAACC TTGAAGTATG CCTTGAACCT ATTAACATGG CCATTATAAG AATAAAATAT 60
GTAGTTGTGT CTTAATGGAA TTAATAAATG TCATTTCACCT AAA 103

40

SEQ ID NO:7664
SEQUENCE LENGTH:211
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

45

CLONE:HUMGS08913
SEQUENCE DESCRIPTION:
GATCAAGGAA TAAAGAATCA TTAAGAATG GGGTGTGGG GGTTCCTTA ATTATCAGTG 60
ACACATTAAT TTTTTCTT AGAGCTTCAT ACAATAACA CATTGCAGAA AGTTTTAGAA 120
AGTTTTGCAG GACCTTAAAT TTTCTGCCCT GACACTTTTC GTCATGTTTC CTGTATTCCN 180

50

55

GGTTATTGTA GCGCATGCTT TTCAGGTAGT N

211

SEQ ID NO:7665

SEQUENCE LENGTH:71

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08914

SEQUENCE DESCRIPTION:

GATCTTAAAT TTTGTGATAT GGAGCCCTGT AATNTTTTTC TTATATAAAA ATGGGTATCT 60
 ATATTCATAA A 71

SEQ ID NO:7666

SEQUENCE LENGTH:344

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08915

SEQUENCE DESCRIPTION:

GATCCCAGCT CATGGCACAG CCGTTTGTAT CCTCGGAAGA ACGGAAGGAA CGATGGGAAC 60
 AGGGCCAGGC TGATTATATG GGAGCAGATT CCTTTGACAA CATCAAGAGG AAACCTTGACA 120
 CTTACCTCCA GTAGAAACAC TGCATTTTTC TGTGAACACA TCCACTTCAC AAGCCTTGTT 180
 TCTGATACTT AGTATCTAGA GCTGGGTTGA GAAAAGTCTG TTACAGTTGC TAGAGGTTTT 240
 CATTAAANCT TATCAGGNGG GCGGCTTTT TAGGATAAGA GGTGAGAACT GGGCAAAAGT 300
 TGTGAAGCAG CAATTCTGTT ATATGGNCAG TGTCTGCTT TTN 344

SEQ ID NO:7667

SEQUENCE LENGTH:200

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08916

SEQUENCE DESCRIPTION:

GATCAGGACT GCTGCACTCC AGCCTGGGTG ACAGNGCGAG ACTCCATCTA AAAAAACAAA 60
 AAGCAAAAAA ACCCACAAAT ACCTCATGGA GATGAACTGT AATAATTGCT TAAAGTTCCA 120
 TTTAATTATG TTAACCTAA TCTAGCAAAA ACATAGATGT ACTTAAAAAT AAATCATGGA 180
 TAATGATTTT TTAACCTAAA 200

SEQ ID NO:7668

SEQUENCE LENGTH:277

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08917

SEQUENCE DESCRIPTION:

GATCTCATTT TCAAGTNTGA GTCTGACCAA CCATGGAAAA TATTCGACAT GAATTAATGT 60
 AGAGAACTAT AAAGCATTTA TGACAGCTCC AAGAAAAGTC ATCTACTCTA TGCAGGAGAT 120
 ATGTTTAGAG ACCTCTCAGA AAAACTTGCC TGGTTTGAGG GTACACAGTA CCATTTTAAT 180
 CTCTGAAAA TATCTGTATT CCTGCTCTGG GGNTGCTGTC ACTGTCAATC TGCTATATTT 240

TTCACTATCC TATTAAAATA TTA CTGTCTC CTTTAAA

277

SEQ ID NO:7669

SEQUENCE LENGTH:163

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08919

SEQUENCE DESCRIPTION:

GATCTTCTAC ATTTATATTT TTAATCTTCT GTTAAATACA CTTTCCGATA TTGCCTTGCC 60
 TTTTGAGCTC TTGCTACAGT CGCCTTTGCT ACTGCTTTAA GAGAATTAC AGGTATTGAT 120
 AAAGAACAAG ACTGTTTTAT TAAAAGNTT ATTCAACTTG AAA 163

SEQ ID NO:7670

SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08920

SEQUENCE DESCRIPTION:

GATCCAAATC TGTTCAAAC ATTCAAAAC TCAAAGATAA TTCATCTTTC GCTAATGCTT 60
 GTGGTTCTGT NGTTCCCTTG AAAAAAATA AAAACCCGAC CCAGCAGCAA A 111

SEQ ID NO:7671

SEQUENCE LENGTH:155

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08921

SEQUENCE DESCRIPTION:

GATCTGTCAC TGTTCCCGT CACCCTCAGA TGGGACCGTC TAGTTGTAGG AAAACAAGCT 60
 CAGGGCTCCC ACTGATTCTA CATTTTGGTG AGTTGTATAA TTGTTATGTA TTGCAATGTA 120
 ATAATAATAG AAATAAAGTG TACGATAAAT GCAAA 155

SEQ ID NO:7672

SEQUENCE LENGTH:239

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08922

SEQUENCE DESCRIPTION:

GATCTGGAGA GGTGTTTGT GAAAGTGGAG AAGATTCACG AAAAGGTCTA AATGAATTGC 60
 GTGTGCAGGG CGCGGATTTA AAGTCCAATT TCTCATGACC AAAAAATGTG TGTTTTTTTC 120
 CCAATGTGTC CCTACCCCCC AATTTCTTGT CCCCTCTTAA AGAGCAGTTG TCACCACCTG 180
 AACACCAAGG CATTGTATTT TCATGCCAG TTAAGTTATT TACAATATTT AAGTTCAA 239

SEQ ID NO:7673

SEQUENCE LENGTH:327

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08923

SEQUENCE DESCRIPTION:

5 GATCCTTTCA TTAATCAGAA CAGCAGCTTA TNAACTGCTT CATTTTCCAA AAGTGTTTCC 60
 CAAAAATCAG AAACCTAAAC ACCCAACAAC AGGAATTATT GCCATCACAT TGGCGTTTTA 120
 CATATGTCAC GAAGTTCACC TAGCTGGTTT TAAATACAAC TTTTCTGANC TCAAGAGTCC 180
 TTTGCACTAC TATGGGAATG CCACCATGTC TTTGATGANT AAGAACGCGT ATCACAATGT 240
 GACTGCAGAG CAGCTCTTTT TGAAGGACAT TATAGAAAAA ANACCTCGTA ATCAACTTGA 300
 10 CTCANGATTG ACTCTACAGA CTCGGAN 327

SEQ ID NO:7674

SEQUENCE LENGTH:377

15 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08924

SEQUENCE DESCRIPTION:

20 GATCTCCNT AATTGGGAAT GAANGATTTC ACAGACTAGA GTCTCCGATG CTGGTCATGA 60
 TGTCAAAAT AAGTCTGAC TCATTAGGG AACTGGATAC TTGGGTCTCC AGAAGGGCCA 120
 ATGGGAGGGC CATAATTCTG TTTATTTTCA AATTGTCTTG TTTTCACCTT GTTAGAATGA 180
 NCTNTGGAAG CCCAGCCAGG GACAATGCAC CTTACAGAG ATTCTGCACT AATCTGAGTG 240
 AAGGTCTAAG GTTTGGAATC TCCCCCTCAT GGAGAGAAGC TTTGTATGGC TGTCATGCTT 300
 25 AGACAGTGAT TCCTGCAACT TGACCTTCAG GCTGGGAGAG GTNGAGAGCC ATGCCTGTTT 360
 CTCCTTNCTT TGCTATN 377

SEQ ID NO:7675

SEQUENCE LENGTH:350

30 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08925

SEQUENCE DESCRIPTION:

35 GATCTGCTTC CCGCAAGACT CACAGCTGTT GGCAGGAGAC CTCAGTTTGT TGCCACATGT 60
 TCCCCTCCAG AGGGCCTCTC ACAACATGGC AGTTATTTGT CCCCAGAGCA AGCAACACCG 120
 GAGGGCAAGG AAGAAGCCAT GATGTTTTTT GTAACCTAGC CTCTGAAAGT GTCATACCAA 180
 TTCTGTATTT TGTTGGTCAC ACAGACCANG TCAACTACAA CGTGGGAGAC TCCTACACAA 240
 GGCATGAATT CTAGGAGGTG GGCATTTTTA AGTGTCTCTT GGAAGGAGGC TGTCACAACC 300
 40 TGGAAGTTAA AAGCATTGAT ATTCTGAAAT ACAGCGTGTA TTACCATGGN 350

SEQ ID NO:7676

SEQUENCE LENGTH:335

45 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08926

SEQUENCE DESCRIPTION:

50 GATCTAGAGG AGGATTTGCA GGAAGAGCTC GTGGAAGAGG TGGTGGCCCC AGTCAAAACT 60
 GGAACCAGGG ATATAGTAAC TATTGGAATC AAGGCTATGG CAACTATGGA TATAACAGCC 120

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AAGGTTACGG TGGTTATGGA GGATATGACT ACACTGGTTA CAACAACACTAC TATGGATATG 180
 GTGATTATAG CAACCAGCAG AGTGGTTATG GGAAGGTATC CAGGCGAGGT GGTCATCAAA 240
 ATAGCTACAA ACCATACTAA NTTATTCCAT TTGCAACTTA TCCCCAACAG GTGGTGAAGC 300
 AGTATTTTCC AATTTGAAGA TTCATTTGAG GGNAN 335

SEQ ID NO:7677

SEQUENCE LENGTH:295

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08927

SEQUENCE DESCRIPTION:

GATCCAAATT TGAAGCTCCA AGGATAGGAA AAAGCTTACT TGTGCCTGTC CTAGACAAGT 60
 ACTAGAGTTT ATATTGAAAT CAAAACCTCT AAAAATAAAA ATCAGTAAGA TTAATTTTAC 120
 TCATTTTCT AACACGAGTC AGTATGCTTG ANGTTTTCAT TGTATTGAT GTCATGTAAA 180
 TTTACTGTAA AAAATAAGAA AANNTTTTAA AATGCTTTAT TGATTAANTT TAGGGTTGCT 240
 TTTCAGTATA CTCAGTAACT CCGAAGTCAG TGTTAACAGT ACTGAGCTTA CATAN 295

SEQ ID NO:7678

SEQUENCE LENGTH:136

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08928

SEQUENCE DESCRIPTION:

GATCTTTTGT TAACTTTTAA ATGGCCTGAG TCCATAGAAA CTGCATCCTG AGAGGTTGCT 60
 CGGCTAGAAA GCGGAAAACC GCTTCACATG AGTGCTCTAC TTTGTAATGA AAATAAACAC 120
 TATTAATACA GGCAAA 136

SEQ ID NO:7679

SEQUENCE LENGTH:310

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08929

SEQUENCE DESCRIPTION:

GATCTGGGAA CGGAAGATGA ATGAATGGAA GATGAATGGT TTCTCTCCCA GTTTCTCTG 60
 AGGCAACAT AATTATACCT NCTCCTTTGT TCTGGGAGGT TTTCTCTTC TCATCTCCC 120
 TCCATTACAC AAAACAGAGT TGGGTCTATA TTNACCCGG CTGGCTCTTG GAACTGCAGG 180
 GAATCCTGGC TGTTTTCATT TTTAAAAAT TATGAGATTA NCTACCAAAC TTGAGATGTA 240
 AGTTGTGGGT TAGCTCTCGG ATTCTGCTAG ATAACCTGGA ACAAAGCATT AACTTCTTG 300
 AGAGCTTCN 310

SEQ ID NO:7680

SEQUENCE LENGTH:177

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08930

SEQUENCE DESCRIPTION:

GATCTGCCAT GTAGGAATGA GACAAATACA GTTTGCTTAT GAAAGGAAAG TGGCATACTT 60
 TTAATTTGGT CTACACAGAA AAGTAAAAGT AAACATTATCA TTTAAATAAG ATTCATTATC 120
 TAATAAATAT TGAGGGAATA TTTTTCCTAA ATAAAAATTT TTCTGACTGC TAACAAA 177

SEQ ID NO:7681

SEQUENCE LENGTH:84

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08931

SEQUENCE DESCRIPTION:

GATCTAAGCT TTCTTTAATA TAAAAAAAT NATACTTCTC TGAAGTGGT AATAGAGCAA 60
 TAATTAAATA CATCTTCTGA TAAA 84

SEQ ID NO:7682

SEQUENCE LENGTH:285

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08932

SEQUENCE DESCRIPTION:

GATCTGTTGG GAAAGATAAG AAAGCTATTC AGGCATCAAT TAGACGTAAT AAGGAAACCA 60
 ACACCGTTTT GGCCAGATTG AATAGCGAAT TGCAGCAACA ATTAAGGAT GTTCTTGAGG 120
 AGAGAATTC CCTGGAAGTT CAACTGGAAC AACTTCGACC ATTCTNTCAC CTATAAGCCA 180
 ATTGCCGTTA ACTGTGAACA TACTTGTTTT TAAGTGTTTT TGGGTTCAAA GCCAATTGG 240
 AGACCTAGAC ATTCAGCTCA CTGCTTAAC CANTATAA TTTN 285

SEQ ID NO:7683

SEQUENCE LENGTH:313

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08933

SEQUENCE DESCRIPTION:

GATCTCAATT CTGTTTCCTC TCACATGATT ACTTGATAGC TAAGCATCTG ATTGGTTTAC 60
 TGCTTTACCA CTGAGCTGAA ATGCCGTGTT TTCCATTAT TAAATCACA CATGGCTCCT 120
 GTTTTNTCA CTCAGCACTT TTTCTCCATA TTCTTCAAGA CGATTGTGAG TATGGTACGT 180
 AACAGGAATT ACATCTGGTA AGTTGTATAG TTTGTGTAG GAACTCTATA TTCATAGCAT 240
 ATTTGTGGAA ATGATACCTA TGGAGGTTTC TCACACTGGT GTGTCATTAT ACATTAATTG 300
 TACAATATGC ATN 313

SEQ ID NO:7684

SEQUENCE LENGTH:110

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08934

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCAGTAAT GGCAAGAGCC TTTNATTCTC GAATGTTTAA AGCCTAGGAG TTCTACAAAA 60
TTGNTTCTT TCTACAAGAN TCCCAAAATG GAATGCCTAA AGAGGTNTNN 110

SEQ ID NO:7685
SEQUENCE LENGTH:132
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08935

SEQUENCE DESCRIPTION:
GATCCCAAAA ACCGGGCAGC CCAGGAAGGA ACTGGGGAAG GTGGTCATTC AGGGGAAGAA 60
CCAGGATGCA GGGCTGGCTC AGGGTCTGCG CAAGATGTTT GGCTGATTAA AAGTTAAACC 120
TTAAAAGAGA AA 132

SEQ ID NO:7686
SEQUENCE LENGTH:85
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08936

SEQUENCE DESCRIPTION:
GATCCCATGC CTGAAATNTG GAAGCATATG TACAAAAATC ATTTTACGT TTTATTTTAA 60
ATAAATCATT GTGTTTGACC GTAAA 85

SEQ ID NO:7687
SEQUENCE LENGTH:333
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08937

SEQUENCE DESCRIPTION:
GATCCTAGTC ATGACTATAC ATTGTGACAT GGTCATTACA TATGGATTAG ACCAACTGGA 60
GAATTGCCAG ACTTGTGGTA CCGATTATAT CATCTCAGTC TTGAATTAC TCACGCTGAT 120
TGTTGAACAG ATAAATACGA AACTGCCATC ATCATTTGTA GAAAACTGT TTATACCATC 180
ATCTAAACTA CTATTCTTGC GTTATCATAA AGAAAAAGAG GTTGTGCTG TAGCCCATGC 240
TGTTTATCAA GCAATGCTCA GCTTGANGAA TATTCCTGTT TTGGAGACTG CCTATAAGTT 300
AATATTGGGN GANATGACTT GTGCCCTAAA CAN 333

SEQ ID NO:7688
SEQUENCE LENGTH:333
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08938

SEQUENCE DESCRIPTION:
GATCTGATTC GCTCCATCAA TGACCCGGAG CATCCACTGA CGCTAGAGGA GTTGAACGTA 60
GTAGAGCAGG TGCGGGTTCA GGTTAGCGAC CCCGAGAGTA CAGTGGCTGT GGCTTTCACA 120
CCAACCATTC CGCACTGCAG CATGGCCACC CTTATTGGTC TGTCCATCAA GGTCAAGCTT 180
CTGCGCTCCC TTCCTCAGCG TTTCAAGATG GACGTGCACA TTA CTCCGGG GACCCATGCC 240

EP 0 679 716 A1

TCAGAGCATG CAGTGAACAA GCAACTTGCA GATAAGGAGC GGGTGGCAGC TGCCCTGGAG 300
AACACCCACC TCTTGGAGGT TGTGAATCAG NTN 333

SEQ ID NO:7689

SEQUENCE LENGTH:110

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08939

SEQUENCE DESCRIPTION:

GATCCATGAA CCTTTTTAT AAGCTGTGTG TGTCTCTGT ATTATTGTTA TTAACATTTT 60
TTTAGNATTT GCCTGTAAGT TATTAAGAC TGATAACTGT AGCTCTTAAA 110

SEQ ID NO:7690

SEQUENCE LENGTH:186

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08940

SEQUENCE DESCRIPTION:

GATCCAGCCA AACGAATTC TGGCAAAATG GCACTGAATC ATCCATATTT TAATGATTGG 60
GACAATCAGA TTAAGAAGAT GTAGCTTTCT GACAAAAAGT TTCCATATGT NATGTCAACA 120
GATAGTTGTN TTTTNNTTGT TAACTCTTGT CTATNTCTCT CTTATATATA TCCNCNTNTT 180
ATCAAA 186

SEQ ID NO:7691

SEQUENCE LENGTH:231

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08941

SEQUENCE DESCRIPTION:

GATCATGTGA CCAATTGTGC ATTCAGTTTT CAGAATTCTT TGCTATATGA TTTGGATTAA 60
TTCTATATAA TTTTGGACTT TTAAATATTA AGGTTAAAAA ATACCTGTAT CTAATAATTGA 120
TTCTGTAAAC TGTGTCTTA AACTAAAGG TATTAAAGTA TAANNITAAA ATTNCAATT 180
TTTTTAAAN NNTTGCAATT TTGATTCTCA TGGGGGAAAT TGGAGATAAT N 231

SEQ ID NO:7692

SEQUENCE LENGTH:277

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08942

SEQUENCE DESCRIPTION:

GATCACAATT TAATAACAAG TAAACTTTA CTTTGGACAA TTTTGCCACT TATTTTGTAA 60
TTTGTAAGCA CACGTTTGAA GATATATTTA TGCCATTAAT ATTTAAGGC ATGTTTAAAA 120
ATTTACTGTT TTCTGAAAAA TTAAATGNNN CTGGTTTGAT TGCTGGAGAT TTATCCAGT 180
TTTNCCTAAA TGTATTTTNA TNCTGTATGG TACATTTTNG NGGATTNCCT GATTAAATGTC 240
ATCTTAGCAT TATATTCTGG TTATCTATAA TNNANN 277

EP 0 679 716 A1

SEQ ID NO:7693

SEQUENCE LENGTH:312

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08943

SEQUENCE DESCRIPTION:

GATCTGGGCA AAGCAAATG AAAACCTTCT GGAAAGGATT CACCATTITA GATGCCATTA 60
 AAAACATTCC TGATTCATGG GAGGAGGTCA AATTGTCAAC ATTAACAGGA GTTTGGAAGA 120
 AGTTGATTCC CNNCCTCATT GATGACTATN AGGGGTTCAG GACTTCAGTG GAGGAAGTAA 180
 GTGCAGATGT GGTGGAAATA GCAAAAGAAC TAGAATTAGA AGTAGAGCCT GAAGATGTAA 240
 CTGANTTGCT GCAATCTCAT GNTAAANCTT TAACAGNTGA GGAGTTGTTT CTTATGGNTG 300
 CGCAAAGAAA TN 312

SEQ ID NO:7694

SEQUENCE LENGTH:83

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08944

SEQUENCE DESCRIPTION:

GATCTTTACT GTTCAGAATT TAGGAAAGTT CTCTGGCTGT TGCATCCAAG TAAATTTAA 60
 ATAAATTTGG TTGCANNTTT AAA 83

SEQ ID NO:7695

SEQUENCE LENGTH:263

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08945

SEQUENCE DESCRIPTION:

GATCCCTTCC TCTGTCTCTC TAACTCCCCA GCCATGAATT TTGGCCCCAG GGAGAGGAAT 60
 AGGCAGTATA GGAGGGATGT CAGGGAATC ACATCTGTGG TTGAATCTCA GAAACAATGG 120
 AAAGGCAGTT GTCTTTGGAT ATGGTGAAAT TGTGGTAGAG CACCCATGGT GGGGGTCTGG 180
 CAGGAGCTCT GCGGCTTCGG TAGCAGCAGT ATGAGGAGAG CTGGGCCACA TGCTTATGGG 240
 TTAGGAGAAG GTAATTTCCA GTN 263

SEQ ID NO:7696

SEQUENCE LENGTH:142

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08946

SEQUENCE DESCRIPTION:

GATCATGGCT GAAAAAGCAG CAAATGCAGC AGGAAAAAG TTCCGAAAGA AGAAGAAATT 60
 TCGCAATTAA GATTTACCA GCAAACTGCA ACATTTTACA TTGCTCCTTT ATTTACTTAT 120
 TAAAGACGTT TGGAAAACTA AA 142

EP 0 679 716 A1

SEQ ID NO:7697

SEQUENCE LENGTH:200

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08947

SEQUENCE DESCRIPTION:

GATCAAGATT GAGAAGACTA GATACATAAC AACCAACTGC AATGTTTGGT CCTTCATTGA 60
ATGGTTGAAC AAACCAGCTG TGAAAGACAT TTTGGGACAT ACAGACATGG ACTGAGAATT 120
AGACATAAGA AAATTATTTT GTTAACTGTT ATCATGGTTA ACAAACGGT CATATAATNT 180
GATTATGTAG AGAAGTTAAA 200

SEQ ID NO:7698

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08948

SEQUENCE DESCRIPTION:

GATCTGCCTG CCTCAGCCTC CCAAAGTGCT GGGNTTACAC GCGTGANCAC CACACCCAGC 60
CTCCATCTTT AAACCTTTAA ATGTGAAATT TCTATCATGT ACCGTTAGCC TAACAAGATT 120
TTNTTTCCTA TTTCTGACTG GTGCCCTTCC CCTTTTtagg AGCAACGAAA GCTACTCTCT 180
TAGTTATGTT CTTGTGATGT GACAAAATGT CAAGAAGATA GGAGAAGAGA ATATTTTATT 240
TCGTTGATGC TTTTGTCCC AAGTGTGACC CTAAACTTAA GCTTTGTAGG AGTTGACATT 300
CTTTCATGTC CCTTCCCTTT ACTCATGCCG AAACATATCAA CTGGGNCATG N 351

SEQ ID NO:7699

SEQUENCE LENGTH:350

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08949

SEQUENCE DESCRIPTION:

GATCTGTTTC TGGGGCCTCT GCGGGTGGCG GCCTGGGGCG GCGCGACGGC TGGTGCGCAG 60
GTACANTGAT GCTGAAGTAC TATGAGCCTT CGGAACCTGT GGAGAGACTA CAANGTTTGT 120
GNNNTATGG TCCCTTTAGT TGGGCTCATA CATTTGGGGT GGTACAGAAT CAAAAGCAGC 180
CCTGTTTTCC AAATACCTAA AAACGACGAC ATTCCTGAGC AAGATAGTCT GGGACTTTCA 240
AATCTTCAGA AGAGCCAAAT CCAGGGGAAG TAGCAGGCTT GCAATCTTCA GGTAAGAAG 300
CAGCTTTGAA TCTGAGCTTC ATATCGAAAG AAGAGATTGA AAAATACCNN 350

SEQ ID NO:7700

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08950

SEQUENCE DESCRIPTION:

GATCCCGCCA GAAATGAATA GACACCGCAA GAAACAAAGC TCGAGTGAAA GCTTGTTACA 60
TAATGATTGG ACTCACAATT ATCGCCTGCT TTGCTGTGAT AGTGTAGCC AAAAGGGCTG 120

EP 0 679 716 A1

5 TAGAACGACA TGAATCCTTA ACAAGTTGGN NCTTGGCAAA GAAAGCTAAG NGGCGTGAAG 180
AAGCTGCATT GGCTGCACAG GCTAAAGCTA AATGNTATTC TAAGTGACAA AGTGTTCAACC 240
TGAATACCAT CCCTGTCATC AGCAACAGTN GAAGATGGGA AAAATNGAAT ATTTACCAAA 300
ATNTCTGCCA TGGTTTTATT TTGGTAACCN GATGCACAAT GTCTTTTTTT N 351

10 SEQ ID NO:7701
SEQUENCE LENGTH:85
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08951
SEQUENCE DESCRIPTION:
15 GATCATATGT GAAGATGTCA ATTAAGCTTG CATTAAAGCCA CCTGCTTTGT AAGTGGATTG 60
ATTAATAAAT AACTTATATT TCAAA 85

20 SEQ ID NO:7702
SEQUENCE LENGTH:89
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08952
SEQUENCE DESCRIPTION:
25 GATCCCAGGG GCTTATCTCT TCAAGTGTGG AGAGGGCAGG GTCCACGCCT CTGCTGTAGC 60
TTATGAAATN AACTAATTGA AAATTCAAA 89

30 SEQ ID NO:7703
SEQUENCE LENGTH:375
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08953
SEQUENCE DESCRIPTION:
35 GATCCAGTGG CAATTGTAAA ACTAGCTATT TATGGCATGC TGCCAAAAAA CCTTCACAGA 60
AGAACATTN ATGGAAAGGT TGCATCTTTT TCCAGATGAG TATATTCCNN CNGATATTCT 120
TAAGAATTTA GTAGAGGAGC TTCCTCAACC ACGAAAAATA CCTAACGTC TAGATGAGTA 180
CACACANGAA GAANTAGACG CCTTCCCAAG ATTTGTGGAC TCCACCTGGA AGATTATCGG 240
CTATAAGAGA ATAAGATTG CAGATAATTA ACAGTGGANG TGATTGAGAC TTTCTNCTTG 300
40 ATGAGTTTCT CTAACCTNCA GGGTGGTGTT AACCAACTGC TACAGTTCAG CACCTGTTTT 360
TNTTGTGCCG NTTN 375

45 SEQ ID NO:7704
SEQUENCE LENGTH:276
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08954
SEQUENCE DESCRIPTION:
50 GATCACATCC TACTTCCTCA ATGAAGGGTC CCAAGCCCGT CCCCCTTCTT CCCACCGATA 60
TTTCCTNGAA CGGGCCCTGG AGTCAGCAAC CAGCCTCTAG CAGCTGCCTC TACGCGCTCT 120

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ACCTGCTTCC CCAACCCAGA CATTAAAATT GTTTAAGGAG AACCACACGT AGGGGATGTA 180
CTTTTGGGAC AGAAGCAAGG TGGGAGTGTG CTCTGCAGCC GNGTCCAGCT ACTTCCTTTT 240
GGAACCTTTA AATAGAATGG GTGTTGGTTG ATTAATA 276

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SEQ ID NO:7705
SEQUENCE LENGTH:220
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08955

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SEQUENCE DESCRIPTION:
GATCCACTGC CATTCTAATT GCTTTAACAA GTCATTACCA CACTACTGTT ACATCTTAAT 60
TATGCATACA GACAGGTAGA CTTGTTTTAC ATATGTGAAC TAACTAGTTG TCAAAGCAAA 120
TGCAGATTGT ATTCTGCAAG TAAAGTCTTT TTCTCTCTGA AATTTCTAGG GATGTTCTTT 180
AAGTGAATTT CATATTAATA CTGAAGATTT TNGTTACAAA 220

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SEQ ID NO:7706
SEQUENCE LENGTH:252
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08956

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SEQUENCE DESCRIPTION:
GATCCAAAGT AACTNAAACA GGAGCCCACA AGACGGTCTG CCAGATTGTN AGCGAAACCT 60
GCTCCACCAA AACCTGAACC CAAACCAAGA AAAACATCTG CTAAGAAAGA ACCTGGAGCA 120
AAGATTAGCA GAGGTGCTAA AGGGAAGAAG GAGGAAAAGC AGGAAGCTGG AAAGGAAGGT 180
ACTGCACCAT CTGNAAATGG TGAAACTAAA GCTGAAGAGG CACAGAAAAC TTGNTTCTNG 240
TNGATTAACG AN 252

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SEQ ID NO:7707
SEQUENCE LENGTH:166
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08957

35

SEQUENCE DESCRIPTION:
GATCTCCTGA CCTCAGGTGA TTCACCCACC TCAGCTTCCC AAAGTGCCGG GNTTACAAGC 60
TTGAGCTACC GCGCCAGCC AACACATCAC TTTTATCTTG CAGCTCCCGA GATTCTCTTT 120
TCTGTGACTN TTAAAATTGT GCTNACATAT GTGTTTGATA TAAATN 166

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SEQ ID NO:7708
SEQUENCE LENGTH:52
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08958

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SEQUENCE DESCRIPTION:
GATCAAAATA TTCTGGAAAA AAATAATAAA AAATAATTTG TATACATTGA AA 52

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SEQ ID NO:7709

SEQUENCE LENGTH:318

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08959

SEQUENCE DESCRIPTION:

GATCATACTN GTGATTATAA AAGNTCCTAG GAGGCTAGAA GAGCCAACCA ACAGAGAAGG 60
GAAAGCAGTC TGTCTGAAC ATAGGGACAT AAGTTCATTG ATGCCAAGTA TCTTCCAGC 120
ATGTTTCTCC CATTIAGAAT ATCTAGCATN TAAGGCCTTT CAATATTAAT ATAAGCCCAA 180
TATCAGCTCT TTCTCTNTGT ATTTTCATCTC TTTCTACTCT CCNATTGTA TTTGGTGTTT 240
CTNTTGAAAG TGTCTATCT GGGAGATGAC CTGCCTATC CTGTNCTATA ACAGTTTNTG 300
NTTGCTGCTG TGTCTTTN 318

SEQ ID NO:7710

SEQUENCE LENGTH:243

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08960

SEQUENCE DESCRIPTION:

GATCCAAGAA ATTACTGAAA TGGACAAGAA ATGTCATTAG TAAAAGCCA TGTTATCTTG 60
AGCACACATA CAGTTAATTT GATAAGAAG AGTATGCCTC TCAGCATTGT GAGATATATT 120
TCAGACTAAT TTGATGTTCT TTAATGTTCC CTTATTTTGG AAACACGTTT TAAATGTGAA 180
ATTAATGTCC TTCACAAAAT GTCTTTTGAA AGCACTGTGA CAGTTGTATA AAGATGATGT 240
AAA 243

SEQ ID NO:7711

SEQUENCE LENGTH:122

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08961

SEQUENCE DESCRIPTION:

GATCTTGGCT TCTGAGGGCT CATTGTAGA GTGGTGAGAA TAATATCTAA CTTGCTAATC 60
TTTCAGAGAC ATTCTGAGAG ACATATGCAA AAGAACTTG TAAATAAAAA GCACTGTACA 120
AA 122

SEQ ID NO:7712

SEQUENCE LENGTH:240

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08962

SEQUENCE DESCRIPTION:

GATCCTTTAT TAAGCTTCTG ATTCATAAAA AAACCTATAA GAGACATTG GGGGGATATT 60
TGGGGAATA GGAAGATGGA ATGGGTAGTA GATAATGTGG TATATTTNAT TTNCTAGAA 120
GTGATAATTG AGTTACGTAG GATAATGTTT TAATCTTAG GAGATGCATG CAGAAGTTTT 180
TTTTTTAAGT TTGAAAAGN CATGATGTTG NCAGCATATT TNCAAATAAN TATGTCCAAA 240

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SEQ ID NO:7713

SEQUENCE LENGTH:110

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08963

SEQUENCE DESCRIPTION:

GATCTGTGTC CAAAAGTGAA CTTNAGTCAG GAATGAATCA ATTTGAGCAT AAACAAGCAC 60
 AAAANTTTAG TCTGCTGGCT GACTGGAAGC AAAAAAGTCA AGATGGNNNN 110

SEQ ID NO:7714

SEQUENCE LENGTH:111

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08964

SEQUENCE DESCRIPTION:

GATCTCAAAA CAATTGTTGC AGCAGGCTCC TGGCAGTCTC AAGCAGTTCA TCTTCTTGGT 60
 GTACTGGTTT CCTATTGTGA TTTTATCATG GAAAAATCAAT TGGCTNNNNN N 111

SEQ ID NO:7715

SEQUENCE LENGTH:309

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08965

SEQUENCE DESCRIPTION:

GATCCTATAG GCAGAGAGTT TTCCTTTCTG ACTTTTCC TTTGCTTTG TGTGACCACA 60
 TGTTTCTGT ACCAGTCACT GGGGAAAGAA GTGAGTTTAT CTCGTTTGT TAAAAAGTTT 120
 TGCTTGCTA TTAGCATTCT CTTTTGGGT CTCAAGATT ATGGAACAAT AAATGTCATT 180
 TAATGCTGTG TGCTTATTTT GAATTCCTCA TCAGGTTTGA GAAGCGGGGT AAAAATACTT 240
 AGATGCTTAT CAGACTTGAA ATTATACTGA GTGGCATTGA ACGTGAGTTT GTCCCAGTGA 300
 ACCAGGCTN 309

SEQ ID NO:7716

SEQUENCE LENGTH:204

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08966

SEQUENCE DESCRIPTION:

GATCCATGAA GCCAGAGCCT GGCTCTGGGT GACAGCAGGA AACGGCTGGG GAAAAGNACA 60
 GCAGGGCGTC CAGCTGAGCC TGCCATTCCA GCCTGTTCCG GGGAAACAGC TCCCAATCCT 120
 AGACTGTGCT GCTCCGGGAG GGCTGCTGGT GGATATTTGG GCTGTTTCA CCATATAGCT 180
 GTCATGAAAA ATGCTTCCGT GAAA 204

SEQ ID NO:7717

SEQUENCE LENGTH:121

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08967

SEQUENCE DESCRIPTION:

GATCTCAGGA ATACAGTCCC ATGCAAAGAT TCTCTGGTTT TATGGCTTTT TTCCCTTTCT 60
TTACACCATC CTCTCCATA AGCACCCATG TTTTGAATA TGAATGTATT TGTAATAATA 120
A 121

SEQ ID NO:7718

SEQUENCE LENGTH:186

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08968

SEQUENCE DESCRIPTION:

GATCACCTGA GGTCTGGGACT AAAAATACAA AAATNAGCTG GGCATGGTAG CCGGTNCCTG 60
TAATCCCAGC TATTNNGGAA ACTNAGAACA AGAGACTTGC TTGACCCTGG GAGGTGAAGG 120
TTGCAGAGAG CCGAGGTAGT GCCACTCCAC TCCAGCCTGG NCGACAGAGT GAAACTCCGT 180
CTCAAA 186

SEQ ID NO:7719

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08969

SEQUENCE DESCRIPTION:

GATCAGCTCT CTGTTTTGGA AAATGGAGTA GATATAGTTC TAGGTACTCC GGAAGACTA 60
GATGACTTGG TGTCAACTGG AAAGCTGAAC TTATCTCAAG TTAGATTCTT GGTCTGGAT 120
GAAGCTGATG GGCTTCTTTC TCAAGGTAT TCTGATTTTA TAAATAGGAT GCACAATCAG 180
ATTCTCAGG TTACCTCTGA TGGAAAAAGA CTTCAGGTGA TTGTTTGCTC TGCCACTTTG 240
CATTCTNTCG ATGTAAAGAA ACTNTCCGAG AAGATAATGC ATTTCCCTAC ATGGGTTGAC 300
TTAAAGGAG AAGGCTCTGT TTCCAGATTN CTGTACACCA TGTGTTNAA N 351

SEQ ID NO:7720

SEQUENCE LENGTH:142

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08970

SEQUENCE DESCRIPTION:

GATCCCAAAG AAGTAACGGG AAAAAGGAAT GTAAGGCATC TCGATAATNT TTTCATATTG 60
ATTACATGTT GAAATANTAT TTTGTATNTA TTGAGTTAAG AAAAATATGT CATTAAAAAT 120
AATNTCACCT GTTCTTTTA AA 142

SEQ ID NO:7721

SEQUENCE LENGTH:130

SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear
 CLONE:HUMGS08971
 SEQUENCE DESCRIPTION:
 5 GATCTTGTGA ATCAAATTCA CAAACATCAG CTTGTTACAA ATCATTNTAT TTATACCCTT 60
 TAAAGAGTGT GGATTTAAGA TTCTTGAAAG GATGTAGNCT ATATANTTTC TCATTCCNTA 120
 TGGTGTAACN 130

10 SEQ ID NO:7722
 SEQUENCE LENGTH:180
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08972
 15 SEQUENCE DESCRIPTION:
 GATCGTTAAT TAATATCTTT CCATNCGAAG AGNAAGCAGA TTTCTTCTGA GATTTCGTAA 60
 CAGTTCCTGG GTGTTCCGG TTCTGCTTCA GTGTACTATC ACTTTGCCTT GCCTCAGTCT 120
 CTCCTTCCTC CGGGGCCACA GAAGGAGAAA GCCCAAAGCA TACCCATCCT GCCCTTTAAA 180

20 SEQ ID NO:7723
 SEQUENCE LENGTH:266
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 25 CLONE:HUMGS08973
 SEQUENCE DESCRIPTION:
 GATCACTGTC CCGNTTCAAA TTATTCTTCA GTCCATTTC CCGGCCTATT TCAGCTGTTT 60
 CTTTTCACCT AACTGTTNAG TCATTNCGGT TTTCAAGCAG TGCTTNATCT CATGTCCTTG 120
 AATATAGTTG TGTACTTTAT TTTNAGGTA ATAATTAGAA CAGTTCCTT CAGAGGCTGC 180
 30 ATTTGCCTTC TTCTGCCACC TAAATATTAC TTCCCTTCAA ATCNGCCTTT GAATCATCNN 240
 NTTTTAAAAA AANTTANCA GNTTTN 266

35 SEQ ID NO:7724
 SEQUENCE LENGTH:33
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08974
 SEQUENCE DESCRIPTION:
 40 GATCAAAGGT ACCATGACCA AATAAGAAAC AAA 33

45 SEQ ID NO:7725
 SEQUENCE LENGTH:219
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08975
 SEQUENCE DESCRIPTION:
 50 GATCTTCTTT TTTNTTCTGG AGCCAGACTT NCTGGGCTTN NATTGCTGCT ATGCTACTTA 60
 CTTGGAAATC TTGGACAAGT TACCTAATTT CTTGTTCTT AAGTTACTTC TGTTGTAAAA 120

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TGATGTGGCC AATAATAGTG CCTATCTCAT AACATGGTTA TTAGAATTAA ACAAGTTAAT 180
 ACTTTTAAAA TGCTTAGAAC AATTGTGGGT ACATACTAN 219

5 SEQ ID NO:7726
 SEQUENCE LENGTH:275
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 10 CLONE:HUMGS08976
 SEQUENCE DESCRIPTION:
 GATCTGTCTG GNAACAGTTT ATGGAAATAT AGATATTCAT GCATCANATA AAAGTGCTGT 60
 GACCATAGAT AAACATGCAGG GAAGTTCTGT NACTGTATCT ACCGAAGATG GTTGCTGAA 120
 AGCCAAGTAT CTTTATACAG AATCATCATT TCTGTCTTCT GCTGCTGGGG ATATTACATT 180
 15 AGGAAAGTGT CATGGNAATA TAACATTACA AAGCAAGANG GGTAGCATCA CAGTNGATT 240
 GTCTTCTGGA TGTCTAAAAG CCTCAACTAA TCAGN 275

20 SEQ ID NO:7727
 SEQUENCE LENGTH:37
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08977
 SEQUENCE DESCRIPTION:
 25 GATCCAGGT TCTCATGAAC CAAATAAGTA ACTTAAA 37

30 SEQ ID NO:7728
 SEQUENCE LENGTH:97
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08978
 SEQUENCE DESCRIPTION:
 GATCTGCCCCA CCTNGGCCTC CCAGAGTGCT GGGATTACAG GCATGAGCCA CTGCGCCCGG 60
 35 NCTGTACTAA GTCTTTTTTT TTTAAATTTT CTCNAAA 97

40 SEQ ID NO:7729
 SEQUENCE LENGTH:284
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08979
 SEQUENCE DESCRIPTION:
 GATCTATGAA CTTCTGCCCC ACATAACTTT TAAAGCAGTA TTTTATAAAC CCCATGAAGA 60
 45 GCTTGCTTTT TTGTCTTTGT AATCCTTAG GGTCTGTGAT ATATGCCAGG AAATCTGATT 120
 GAAACTAATA TGCTTTTAT TCTCCCATTA TTCCCTAAAT NGTTATATCA CAGGCACTTG 180
 CCTACATTGG GAAAGTAAGG ACAAATAATA CCCATTTAAA GAACTNGCC TATTATTNNG 240
 ACTGTCTTTC GTAAGCACTT GCTGAACNGC TGACTTAACT CAGN 284

50 SEQ ID NO:7730

55

SEQUENCE LENGTH:374

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08980

SEQUENCE DESCRIPTION:

GATCTCGCAA TGGGGAAGGC CCTGGTCGAC CAGAGGGAGC TGTACCTGGG CCTGCTCTAC 60
 CCCACGGAGG ACTACAAGGT ATACGGCTAC GTCACCAACT CCAAGGTGAA GTTTGTCATG 120
 GTGGTAGATT CCTCCAACAC AGCCCTTCGA GACAACGAAA TTCGCAGCAT NTTCCGGAAG 180
 CTACACAACCT CCTACACAGA CGTGATGTGC AACCCCTTCT ACAACCCGGG GGACCGTATC 240
 CAGTCCAGGG CCTTTGATAA CATGGTGACG TCGATGATTG ATACAGGTTG TGCTGAGTGA 300
 GCTGTGCTGC CAGCCATCGN AGAGGAGCCC NTNGCACGAC TTGTGGTGGG GTCCGTCGGT 360
 CTTGTTTCTN TTTN 374

SEQ ID NO:7731

SEQUENCE LENGTH:164

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08981

SEQUENCE DESCRIPTION:

GATCCGGTTG GACTCTGACA TCGGATGCCC TCAAACATAC AGAACTTCCA AACTCAAGTC 60
 CAGCCATAAG CTATTTTGCC AACATGTCAG AGTAATCTGT ATTTTGTAT GTGATTCTA 120
 CTTTATAGA CTTGTTTAA AACATAAAA CACATTTTA TAAA 164

SEQ ID NO:7732

SEQUENCE LENGTH:287

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08982

SEQUENCE DESCRIPTION:

GATCTTTCAT GAAAATTAAT TGTGCCCATG TCCAAGTTTG AATTAGAGAT ACACAGCACA 60
 CAATCATTTT TGTACCCTT TTTGGAATAT CTAGCATTAG CCTTGATAGT TTTGTGTGGT 120
 GTGTTTGTAG TATATCTGAN CTGTTAGTTA TATTTGGTTA ATTTATIAAA NGATGTGTGT 180
 TAANCCTTAA TATTTATGCA GTGTTAAGT ATTTGGAATA TATTNGAAAT AAATTATCCA 240
 GTGTTTTAGA TAAATGGTTA TTAAATTGCN NAANGTGATT CTCTAAA 287

SEQ ID NO:7733

SEQUENCE LENGTH:173

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08983

SEQUENCE DESCRIPTION:

GATCTGTGCC GTTCAATAGG CATCGTCTCT CAGCCTGAGG GAGGCTGGAT TCTGGGTTC 60
 TGTAATCACA GGGAGGAAAA GCTTTCTTAA AAATGGACAT GTATGTCCGT GTNAGTGTGT 120
 GTGTAGATTT ATAGTTTTTG GTAGTGGCAG GAATAAAAAA AATCCATCCT AAA 173

SEQ ID NO:7734
 SEQUENCE LENGTH:198
 SEQUENCE TYPE:nucleic acid
 5 TOPOLOGY:linear
 CLONE:HUMGS08984
 SEQUENCE DESCRIPTION:
 GATCTCTATT TTGTGCCAG ACTCTGAGCT GCTTTATGAA CACCTCAATT AAATNACTTC 60
 10 ATTGGAGTGA TTTGAGTAAT CTATCTATAG TGTAATATTT TCTATGAATA ATTTTCTGTA 120
 ACCTTATTTT ATAAGTTAAT ATCTAAAAAG TGTTTATTTT CAAATTGCCA AATAAAAGGT 180
 TTTATATTAG TCATTAAA 198

SEQ ID NO:7735
 15 SEQUENCE LENGTH:94
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08985
 SEQUENCE DESCRIPTION:
 20 GATCTAGAGA CTCATTCAAT AGCAATGTGA CCTTTTAAAT ACTTACATTA AGTAAAACTG 60
 CCAGTAGATT AAATCATATA TATATATATA TATN 94

SEQ ID NO:7736
 25 SEQUENCE LENGTH:363
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08986
 SEQUENCE DESCRIPTION:
 30 GATCACCTGN ACTCCAGCTC AGATTGCCTC TCCTGGACAT GGCAATGAAT GAGTTTTTAA 60
 AAAACAGTGT GGATGATGAT ATGCTNTTNT GAGCAAGCAA AAGCAGAAAC GTGAAGCCGT 120
 GATACAAATT GGTGAACAAA AAATGCCCAA GGCTTCTCAT GTCTTTATTC TGAAGAGCTT 180
 TAATATATAC TCTATGTAGT TTNNTAAGCA CTGTACGTAG AAGGCCTTAG GTGTTGCATG 240
 35 TCTATGCTTG TGGAACTTTT CCAAATGTGT GTGTCTGCAT GTNTGTTTGT ACATAGAAGT 300
 CATAGATGCA GANGTGGTTC TNCTGGTACG ATTTGATTCC TGTTGGGATG TTTTAACTAA 360
 NAN 363

SEQ ID NO:7737
 40 SEQUENCE LENGTH:262
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08987
 45 SEQUENCE DESCRIPTION:
 GATCTTCTTT GATGATGAGA GGCGGAATAT TGTAGACGTC AGCAAACTGG GTGTTACCTG 60
 CATTACATC CAGAATGGAA TGAATCTTCA AACTCTAAGT CAAGGGTTAG AGACATTTGC 120
 AAAGGCCCAA ACTGGGCTT TAAGGTCCAG CCTTGAGGAG AGCCCATTTN AGGCCTAAAC 180
 TGAAAGGAAA TCAAGAAGGC ATTTTCAGGT GCATTTGTAA TTTATTAAAG TTCATCTGTG 240
 50 TGTGACAGAA AAAAAAAGTA AA 262

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SEQ ID NO:7738

SEQUENCE LENGTH:361

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08988

SEQUENCE DESCRIPTION:

GATCTGTGCC ACATGGAGGT TTTGGGATGG GATTNAAAG CTACCTGCAG TGCATCTTGG 60
 GTGTTGACAA TATCANAGAT GTTATCCCTT TCCCAAGGTT TCCTCATTCA TGCCTTTNAT 120
 AGCTGGAAGA TTGGTTAAGG CAAAGCACCC CCCATGGCAG AGACACTGCA CATGATTGTN 180
 CATACAGCAG AATGCATGTT TGGATTNTAG AAATGCAGAT TTCAATATGT AATTGTTGTG 240
 CCATAAGATA TCATAGNAAA NNTATAAGTG GTTGTNCTTT TCTTAGAAAG TTGAGGGTAT 300
 TTCACGTAAG GATGAGCTCC CGCAAGNNGA GGTACTTNTT AGCANGGGGA CTCTCAATCG 360
 N 361

SEQ ID NO:7739

SEQUENCE LENGTH:143

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08989

SEQUENCE DESCRIPTION:

GATCTTGATG TGGGTGATAG TTTTACTTAT GTACATCGAT ATACATCTAT TAAAAACAT 60
 GTACATTAA ATTGTTGCAT TTTATGTATT TAAAATTAT TGAGTANTCC TTCTGTATGT 120
 ATTATTAAAG AGAATATAGC AAA 143

SEQ ID NO:7740

SEQUENCE LENGTH:333

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08990

SEQUENCE DESCRIPTION:

GATCATAGAG TTTGGCTGGG GAGGGGGGCA GTTTAGAGG CTTCCTTG GTGTTCTCA 60
 GAATGATATC TCTTACTCCG GGGGCCAAGG TAGGGGTTAG CTTTGTCT CTTGTAGTT 120
 TAGATTGTAT CTCCTGCCTT GTTCAAGTTC ACAAATCTTT TTGTGTATAC ACATATGTAC 180
 ATGAAAAATNA TGTTGATGCT TTTAATTATT TTACCCITCA TTATTCATT TTNATAGTT 240
 CTCATAGCTA TGTCTTTCAG TTCCTAATC TTTTTCAC AGTGTTAAT CTGTCATTAA 300
 ATCCCATCCA AAGTATGTTT TCTCTCAGAA GAN 333

SEQ ID NO:7741

SEQUENCE LENGTH:135

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08991

SEQUENCE DESCRIPTION:

GATCCTTGTA CACTGTTTAT ATGTGCAATA AAATGCATGG CCAGCTGACA GTATCGTCAG 60

TGGACAGAAT GTATATAGTG CAAATATCCT TCCTTTTATT ATTTAACAGC CATTAAAAATC 120
TTGGATTTGT AAAAA 135

5 SEQ ID NO:7742
SEQUENCE LENGTH:333
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
10 CLONE:HUMGS08992

SEQUENCE DESCRIPTION:

GATCCCAAGT CACAATTATT CACCGGGTAT TTAGTTATTC ANAGGCTGCT CTGCTGAGAA 60
GNTGAACAAA TTTCTTGTCC AAAACAATGT ATTTCAAACG TGCCGCTCGG GCCTTTCCCG 120
TATTGCTCAC TGGTGCTGGG AAGACAACAC TTCTGAACTA TATTTTGACA GAGCAACATA 180
15 GTAAAAGAGT AGCGNNNNCT TTAAATGAAT TTGGGGAAGG AAGTGCCTG GAGAAATCCT 240
TAGCTGTCTAG CCAAGGTGGA GAGCTCTATG AAGAGTGGCT GGAACCTAGA AACGGTTGCC 300
TCTGCTGTTC AGTGAAGTGA GGAATGTGTT TTN 333

20 SEQ ID NO:7743
SEQUENCE LENGTH:219
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08993

SEQUENCE DESCRIPTION:

GATCCCAACT GTATAACATT CTGAAAAAGG CACAACTATG GAGACAATAA AAAGAACAGA 60
GTTTTGGATG AAGGGAGGGA TGAACAGGCA GAATACAAAC AAATTTTAGG GCAGTGAAAC 120
TATTATTATG ATACTTTATG GATATAGAAT ATTATGCATT TTTCAAAACA CATAGAATAT 180
30 ACAACATGAA GAATGAATGC TAATGTAAAC TGGATTTTN 219

SEQ ID NO:7744
SEQUENCE LENGTH:59
SEQUENCE TYPE:nucleic acid
35 TOPOLOGY:linear
CLONE:HUMGS08994

SEQUENCE DESCRIPTION:

GATCTTGGGC CACACATGAA AATACTAA CACTAATGAC AGCTGATGAG ATGCTTAAA 59

40 SEQ ID NO:7745
SEQUENCE LENGTH:353
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
45 CLONE:HUMGS08995

SEQUENCE DESCRIPTION:

GATCAGAGTG ATGCTGGAAC TCAGTGTGCA TAAAATTTCA GTCAGTGAAT ATCACTGAAC 60
GTCATATACT ACTTGGTATG TGACTTTGGT TTGTGTTAAG AAAGCTTGTA TATAATATTT 120
50 TTNGCCATAG TAAGTGAGAA ATTGTCCTTA ATCATGCCTG TTTGATGGTA CTAGGAAAGA 180
AAGGGGTAGA GATTAATTCT TGCACAGTAT AAGCAACAGT GCAACAACT ATGCCATTN 240

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CCTTTTNCCT CTTACTTGAA GGCAGAATCG CAAAACGTTT GANATGGCTT TCCTAAACTA 300
CTCTACTCTG GTGNGAGCTC ATTTACCACA NGAAGCCTTA TAACACCGTT TNN 353

5 SEQ ID NO:7746
SEQUENCE LENGTH:327
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08996
10 SEQUENCE DESCRIPTION:
GATCAGGTGA TTGCCTTTCT CAGCTGTCAG TTCTCTAATT TCAGGCTTGG TAGCTTGTAG 60
GAACTGAAAT TGCAATTAAA ACCTTTATAA ACTCAAACTA AATCATGAAT TACAGAAAAA 120
GTCCATTCTT CCAAACTTG ATGTTACCAC ACTTACAAGT TAAAAATATG AAGTCGACTG 180
15 TTAAAGGAT TCTGCATATA TTCTAGTGTG CACATTCAGA AACATTTTTC TTGGAAAAAG 240
TACCCAACAT TTTTATAAC TGCACATATT AATTTATTGC CAGAATAAAT TGCATTGCAT 300
GCTAAATTAA NGTCAGATAN TTCNAAA 327

20 SEQ ID NO:7747
SEQUENCE LENGTH:153
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08997
25 SEQUENCE DESCRIPTION:
GATCATGTAA ACTTGCTGTT TTNGTTTTTN CCTGCCGGGT GTTGTATGTG TGGTGACTTG 60
CGGATTTATG TTTCAGTGTA CTGGAACTT TCCATTTTAT TCAAGAAATC TGTTCATGTT 120
AAAAGCCTTG ATTAAAGAGG AAGTTTTTAT AAA 153

30 SEQ ID NO:7748
SEQUENCE LENGTH:41
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
35 CLONE:HUMGS08998
SEQUENCE DESCRIPTION:
GATCTTAATT TTGTTTTTGG TTAAAAATAG TGTTTCCTTT N 41

40 SEQ ID NO:7749
SEQUENCE LENGTH:299
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS08999
45 SEQUENCE DESCRIPTION:
GATCTATCTA AATGCCGATT TGAGTTCGCG AACTATGTA CTGCGTTTTT AATTCTTGTA 60
TTNANACTAT TTAATCCTTT CTTACTGTGCG CTAAATATAA TTGTTTTAGT CTTATGGCAT 120
GATGATAGCA TATGTGTTCA GGTTTATAGC TGTTGTGTTT AAAANTTGAA AAAAGTGGAA 180
50 ANCATCTTTG TNCATTTAAG TCTGTATTAT AATAAGCAAA ANGNTTGTNT GTATGTNTGT 240
TTNATATAAC ATGACAGGCA CTAGGACGTC TGCCTTTTTN NGGCAGTNCC GTTAAGGGN 299

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EP 0 679 716 A1

SEQ ID NO:7750

SEQUENCE LENGTH:169

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09000

SEQUENCE DESCRIPTION:

GATCAATTAG ACATTTTGAA AATAATTTAA AGTGTTCCT TTAATGTTCT CTGAAAACAA 60
GTTTCTTTTG TAGTTTAAAC CAAAAAAGTG CCCTTTTGT CACTGGATTG TCCTAGCATT 120
CATGATTTT TTTTCATACA ATGAATTAAT ATTGCTAAAA TCATGGAAA 169

SEQ ID NO:7751

SEQUENCE LENGTH:53

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09001

SEQUENCE DESCRIPTION:

GATCATTAA TGAATCTCA AGGACTAATG AAATAAATGC TAGACTGCTG AAA 53

SEQ ID NO:7752

SEQUENCE LENGTH:252

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09002

SEQUENCE DESCRIPTION:

GATCCTGAAA ATAAACTAA CACTCCAGTA TTTTGTTCATT GTTTTCGCA ATTGAGCTAT 60
CTGAAACTG TTATTCCTAA GTAATGTTCA AAAATGATAA GTAATCTGGA TACCTTTTTC 120
TTATACTTTC TCCTAGGAAA ACTTTAAAC TTAAAAAGG CAAACCTACC AATAGGAATA 180
ACANATTAAT TGTCAAGAGA GTATATCCAA TATTAGGATA TAANTGTATG TGTCTCAAGT 240
TTAACTCTAC AN 252

SEQ ID NO:7753

SEQUENCE LENGTH:237

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09003

SEQUENCE DESCRIPTION:

GATCTACAAA AAATTCCTGG AGCCATATAT ATACCCTCTG GTNTCCCAT TCGCTAGTCG 60
TATATNGCCT NAGAAAGCAA TACAAGAATC CAATAATACA AACAAAGGCA NAGTAAACTT 120
TAAGGGNGCA GACATGAATG GCTTACCAAC AAAAGGACCA NCAGAAATCT GTGATAAAAA 180
GAAAGACTAA AGAAATTTTC CTAAAGGACC CCATCATTTA AAAANTGGNC CNGGNNN 237

SEQ ID NO:7754

SEQUENCE LENGTH:264

SEQUENCE TYPE:nucleic acid

EP 0 679 716 A1

TOPOLOGY:linear

CLONE:HUMGS09004

SEQUENCE DESCRIPTION:

5 GATCTTCCCA AACCCAGAGA AAGACATCAA TTTCCAAGAA CAAGAAGGTT ATCAAACACC 60
 AGGCAGATTT AACCCAGAGG ATACTACCTC AAGGCATTTA ATAATCAAAC NNCCAAAAGT 120
 CAAGAATAAG GAAATAATCC TAAAAGCAGC AAGAGAAAAG AAACAANTAA TATACANTGG 180
 AGTTCCACTA TATCTGGCAG CAGACTCTTC ATTGGAAACC TTATAGGCCA GGNGNGAGTG 240
 10 GCATGACACA TTTAANGTAC TGGN 264

SEQ ID NO:7755

SEQUENCE LENGTH:286

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS09005

SEQUENCE DESCRIPTION:

20 GATCCAGAGC TGTTCCTGT GACAGCGGTT TCTNTGGATG TCAAAGGCAG CTGCCTGGTT 60
 GCCCAGCTTG CTTCCTGACT GGTGGCCCTT ATGGGTGGGT GTGCGATGGA AATNTGTTCC 120
 TGCCGGAGTC TGAGGCACCA GGGTGTGCTC AAAGGCTGGC CCTGGTGGTG GACTGGCACC 180
 TGTGCAGAGT GCCGTGTGCT TGTGGTGC GC CATCTGAAGC AAGAGTCCAG CGTTCTGCCG 240
 TGTCTGTCCC CCACCATGCC CCTACAGGC GGTACTGATG GCGCTN 286

25 SEQ ID NO:7756

SEQUENCE LENGTH:382

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

30 CLONE:HUMGS09006

SEQUENCE DESCRIPTION:

35 GATCCTTTTT CCTTCAGCAG CATTTCTTAC TGGCTGTGGC TGGAATCTGC CTTTAATCAC 60
 AGCTGTCACC ATTCTCACGT GATTCTTGTG AGACTCTTTT TGGTTATAAT TACTATTTAA 120
 TATTTAGACT ATTTTACTGA GCAGACTTTA TAAATGAGAT ATCTACAAGG CACTTAAAGT 180
 GTTACAGATG TTTTACCTTA AGANTTATTT AAGTNGTGTT GGGTTAAGAC AGTTTTCAGT 240
 GTACCGTAAA TGTGTGTTTT TCAGAAAAAG ACAAACGAT GGTGCTGACT GGTTTTCTGT 300
 ATATNGCACA ACAGTCCTCA AATACACTGG ATGTATGGAA CCTNTTCCTT NCATCCAGGC 360
 AGCATTTTTN TTNCNCTCTN CN 382

40 SEQ ID NO:7757

SEQUENCE LENGTH:298

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

45 CLONE:HUMGS09007

SEQUENCE DESCRIPTION:

50 GATCATCTTT GAGTAGCACT GTTTGGGGC CCTCGGTCTC TCTGAAGACC CTAGCAGAAC 60
 TGATACCTAC CTGTATCTCT TGTCTCTCC TATTTAGATT TCACCTCCAG AGAAGTTGTT 120
 CTTAGCAAG AATGTGTCAC TAGTAAGGAC ATCTCTAGCA TTTCTCTAGC CTTCTTTTC 180
 TGCTGCTCAA AAATAATCGT TACAAAGCTT AGGTTTAAGC TGTATATGAA ATATTTATGC 240

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GACTCTCAAA CTTTAAAGGA GTTGCTCCTT TGTTCACAAA TTAAATGTGT TAGATAAA 298

SEQ ID NO:7758

SEQUENCE LENGTH:292

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09008

SEQUENCE DESCRIPTION:

GATCATGGTC TTCAAAGATG TAAATACAAG AGAACCAAAG TTATTCCGGG CAGTTCAGAG 60
TTCAGAACGT GTTATTCTCT CCAGAACGAC AACGCCATAT TTCCTTTGAG GCCTTCGCCC 120
ATCCTGCTGA CCCATTTTNN TGCCCTCTTC TTACCCCAAT TTTNTTGTAT TACCTCTAC 180
AATATACTTT TNATTGAGCA CTTTGCTGCT GAAATGCTGC CTCTTGCCTT TTTTTTTNA 240
AATTTAAAT TATCTAAAT TATGGTTTGT GGTGGTGTCT ATNGCAAAGT TN 292

SEQ ID NO:7759

SEQUENCE LENGTH:307

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09009

SEQUENCE DESCRIPTION:

GATCTGTAA TGAAAAGTGC TGGAAATACCT CAACCAAGAA AAGGCAGAAA AGGGAAGGGA 60
GCATATTGCT AAGAGAGCAA TGGAAAATAT GTAAGCTGCT TTCATTAATT ACCCTACTTT 120
CATTCTCCC ACCCCAAGCA AATCCCAACA TTTCTCTTCA GTGTGTTGAC TTCTATCTTG 180
TTAACTGT AATATCTTTA AATGATGTAC AGGCAGATGA AACCAGGTCA CTGGGGAGTC 240
TGCTTCATT CCTCTGAGCT GTTATCTTGT GTATGGATAT GTGTAAATGT NGGTGACTCC 300
TTGATAN 307

SEQ ID NO:7760

SEQUENCE LENGTH:165

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09010

SEQUENCE DESCRIPTION:

GATCTCTGAA CATGAAAACC AAGGTGGCTA TTTTCAGGT GCTTTCAGCT CCAAGTAGAA 60
ATAACCAGAA TTGGCTTACA TTAAAGAAAC TGCATCTAGA AATAAGTCCT AAGATACTAT 120
TTCTATGGCT CAAAAATAAA AGGAACCCAG ATTTCTTTCC CTAAA 165

SEQ ID NO:7761

SEQUENCE LENGTH:334

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09011

SEQUENCE DESCRIPTION:

GATCGATGAC GCAGGTCCTT CCAGTGAAAT GAATGGTCTC AAAAAATGGA GAGGATGTGC 60
TGGGGATTTA GAAGGCAGGG TAGCCAGAAA GAAGCACAAA TTACCCCCAC CATAAGCTTC 120

ACAGAATTGC TGACGCTAAC GGCCATGGGT GAGATTTTGG CAATAAGTGT CAGCCTGATG 180
 ACAGATACCA CAGACAGTTG CAAAAATGTC CAAGTTTCTC CTGAAATTTT CTGGCAGGGC 240
 AGTGGGCTCC ATCCTTAGGA GTGAATCAGC TTTGGTGAGT ATCGTGATTG AACAGAGCCT 300
 5 TAACACCAGG GCCCCCTTAA CTCCGCACTC CTTN 334

SEQ ID NO:7762
 SEQUENCE LENGTH:247
 SEQUENCE TYPE:nucleic acid
 10 TOPOLOGY:linear
 CLONE:HUMGS09012
 SEQUENCE DESCRIPTION:
 GATCGCTTTG ATTTTAAAGT TCATTGGAAC TACCAACTTG TTTCTAAAGA GCTATCTTAA 60
 15 GACCAATATC TCTTTGTTTT TAAACAAAAG ATATTATTTN GTGTATGAAT CTAAATCAAG 120
 CCCATCTGTC ATTATGTTAC TGTCTTTTTT AATCATGTGG TTTTGTATAT TAATAATTGT 180
 NGACTTTCTT AGATTCACCT CCATATGTGA ATGTAAGCNC TTAACATATGT CTCCTTTGTAA 240
 TGTGTAN 247

20 SEQ ID NO:7763
 SEQUENCE LENGTH:312
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 25 CLONE:HUMGS09013
 SEQUENCE DESCRIPTION:
 GATCCTTCCT GAGCGTTTCC TGGCAGTTTT AAAACGAAAA ATCAGTGTTA AGTTTGATGC 60
 AGTTATTGGA TATAAAATGA AAGCGCAATA AGCACCTAGT TTTCTGAAAA CTGATTTACC 120
 30 AGGTTTAGGT TGATGTCATC TAATAGTGCC AGAATTTTAA TGTGAGNCT TCTGTTTTTT 180
 CTAATTATCC CCATTCTTC AATATCATTT TTGAGGCTTT GGCAGTCTTC ATTTACTACC 240
 ACTTGTTCTT TAGCCAAAAG CTGATTACAT ATGATATAAA CAGAGAAATA CCTTTAGAGG 300
 TGACTTTAAG GN 312

35 SEQ ID NO:7764
 SEQUENCE LENGTH:93
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 40 CLONE:HUMGS09014
 SEQUENCE DESCRIPTION:
 GATCTGCCTG TCCGGGCTGG GACAGAGACT CCCCAAGNAC CCCATTCTGC CTCCTTCTGG 60
 GGAAATAAAT AAGTGTCTGT TTCAGCAGCT AAA 93

45 SEQ ID NO:7765
 SEQUENCE LENGTH:133
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 50 CLONE:HUMGS09015
 SEQUENCE DESCRIPTION:

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GATCTGGCTA AGCATCTTCC TCATGCTTTC AGTAAATTGG AAAACCCACG GAGGTAAAT 60
 ATTACCTTTT TTTTITAAA CTAAANCAA TNCTGTTTAT TTTTNNATTA CATTNCCCA 120
 TATGNGNGGA ATN 133

SEQ ID NO:7766
 SEQUENCE LENGTH:300
 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09016

SEQUENCE DESCRIPTION:

GATCGTNAAA ACCCCAAATG GACTTATTTT AAGTCACTTG CCAAATGGCC CAACTGCTCA 60
 TTTTAAAAATN AGCAGNGTTC GTCTTCGTAA AGAAATTAAG AGAAGAGGCA AGGACCCAC 120
 AGANCACATA CCTGAANTAA TTCTGAATAA TTTTACANCA CGGCTGGGTC ATTCANTTGG 180
 NCGTATGTTT GCATCTCTCT TCCCTCATAA TCCTCAATTN NTCGGNAGGC AGGTTGCCAC 240
 ATTCCACAAT CAACGGGATT ACATATTCTT CAGATTTCAC AGATACATAT TCAGGTGTGN 300

SEQ ID NO:7767
 SEQUENCE LENGTH:105
 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09017

SEQUENCE DESCRIPTION:

GATCAAAGTA GCCACAACAT TCTCTTAAGC CAAAGNCCAA TCCAGAACAA NGCCCTAACT 60
 CTCTTCAATT CTATGAAGAC TAAAAAGTA AGGAAGCTNC AGANN 105

SEQ ID NO:7768
 SEQUENCE LENGTH:216
 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09018

SEQUENCE DESCRIPTION:

GATCGTCAAA CCATTCATCC TTTTAAAGGT TTATTTGAAG ATGCTGTAA AGTACAGAAT 60
 TTTGTGTACA GGTAGATTTT TCCGTCCCTC ATTAATAGTG CCTTCTTAAT TAATACAGNC 120
 TGGTGTTAGC TATAACAAGG CNCCAGTAAG GCCAAAGAAT CCCAAGTTCT TTGTGGAAAA 180
 ANAAAAAANN NCTTTTGGGG NCAGNTTTC CTTCN 216

SEQ ID NO:7769
 SEQUENCE LENGTH:75
 SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09019

SEQUENCE DESCRIPTION:

GATCCTCCCG TGTGTGGTTG GAAAACTTTT GTTTTTTGGG GTTTTTTTTT TCTGAATAAA 60
 AAAGATNCTA CTAAT 75

SEQ ID NO:7770

SEQUENCE LENGTH:341

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09020

SEQUENCE DESCRIPTION:

GATCTGTGTC TTAATTGTTT AGTTAGAGTG AGAAGTTGAC CTATGATTCT TTTTAAATT 60
 TTATATTGG AACAAAGCTG CAAGTTATGG TAANGTACTG TACTGNGNGA NGTATTATGA 120
 TATTTAATGC ATCTNTGGCT TAACACTTGT GAGAGTTACC AGCTTGAAAA TGATGGTGGT 180
 GACTACCTCT TGANTCACAT CTATCAACCA CTGGCACCTA CCACCAAGCT GGCTTCAATT 240
 AGTATGTGTT GCTTTTGGT ATTAACANCT AACCGTACTA GAGACCAAAG TGAACCCTGA 300
 TTTTAAATAT GTNTTAAATA ATGGTGGTTT TATCTAGTGG N 341

SEQ ID NO:7771

SEQUENCE LENGTH:238

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09021

SEQUENCE DESCRIPTION:

GATCCAAGCC TGGAGTTTGC AGAAGATACT GTCCTAATAA GCAGGCATTT CTAAACCAAG 60
 TATCTAAGCC TAAGCACAGC TTGTCCTGGG TGAAATGTCT GCCACAAAAG ATAGTTTCTC 120
 CTAGCTCAGA CTTAACCATT TATAAAGGTT GGTAAATAC TGGCAGTGAC AACAAATTGA 180
 CTTTTTAATT TTTTATTG CATTATTCCA ATAAATGAAA ATCTGTCAGA GTTCTAAA 238

SEQ ID NO:7772

SEQUENCE LENGTH:123

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09022

SEQUENCE DESCRIPTION:

GATCTGCCCC CACTGTCCTG TGAGGACAGC TGAGGCCAAG NAGTGAAAAA CCTATTACTA 60
 CTAAGAGAAG GGGTGCAGAG TGTTTACCTG GTGCTCTCAA CAGGACTTAA CATCAACAGG 120
 AAA 123

SEQ ID NO:7773

SEQUENCE LENGTH:361

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09023

SEQUENCE DESCRIPTION:

GATCCAGGTA GAATTTTNA ACCAATCAAA TGAAAAAAAC AAACAAACAA AAAAGGAAAT 60
 GTCATGTGAG GTTAAACCAG TTTGCATTCC CCTAATGTGG AAAAAGTAAG AGGACTACTC 120
 AGCACTGTTT GANGATTGCN TCTTCTACAG CTTCTGAGAA TTGTNTTATT TCACTTGCCA 180
 AGTGAAAGGAC CCCCTCCCCA ACATGCCCA GCCCACCCCT AAGCATGGTC CCTTGTCAAC 240
 AGGCAACCAG GAAACTGCTA CTTGTGGNCC TCACCAGAGA CCAGGAGGGT TTGGTTAGCT 300

EP 0 679 716 A1

CACAGGACTT CCCCCACCCC AGANGNTTAG CATCCCATAC TAGACTCNTA CTCAACTTNN 360
N 361

5 SEQ ID NO:7774
SEQUENCE LENGTH:54
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
10 CLONE:HUMGS09024
SEQUENCE DESCRIPTION:
GATCAAGCGA ACTAATTTTA GGTGAAATC CGAATAAAAG AACTTTACTG GAAA 54

15 SEQ ID NO:7775
SEQUENCE LENGTH:188
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS09025
20 SEQUENCE DESCRIPTION:
GATCTGTATA ATGTACATTC AATATAGAAA GCTTTATATA TTTAAAAGNG TATAGAACAT 60
TTNACAATTA CACTCATCTT TAACATAACA TCTTGACATC CATTTTNAAG TTTTGTGCA 120
CAAGCTCCTT TNCATTCAAT TTGGTAAAGC CAGTTATACA TACTANTGTG TACTGTGAGC 180
TTTCAGAN 188

25 SEQ ID NO:7776
SEQUENCE LENGTH:221
SEQUENCE TYPE:nucleic acid
30 TOPOLOGY:linear
CLONE:HUMGS09026
SEQUENCE DESCRIPTION:
GATCACCTGN AGGTCAGGAA GTTTGAAAAC CAGCCTGGCC AACATGGCAA AACCTGTCT 60
CTACTAAAAC AAAAATNAGC CAGCATGATG GCAGGCGCCT GTAGTCCNNN CTATTCAGGA 120
35 GGCTGAGGCA GGAGAATCGC TTGAACTGGG AGAGGGGCAG AGGTTGCAGT GAGCTGAGAC 180
TGCATTCCAG CCTGGGCGAC ACAGCAAGAG TCTGTCTCAA A 221

40 SEQ ID NO:7777
SEQUENCE LENGTH:200
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS09027
45 SEQUENCE DESCRIPTION:
GATCGTAGGA ATTGAAGGAG TGTCCCGCCT TGTGGCTGAN AACTGGACAG TGGCAGGGGC 60
TGGAGATGGG TGTNTGTGTG TGTGTGTGTG TGTGTGCGCG CGCGNCAGTA 120
CAAGACCGAG ATTGAGGNAA ANCATGTCTT CTGGGTGTNA CCATGTTTCC TCTCAATAAA 180
GTNCCCCTGT GACACTCAAA 200

50 SEQ ID NO:7778

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EP 0 679 716 A1

SEQUENCE LENGTH:286
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 5 CLONE:HUMGS09028
 SEQUENCE DESCRIPTION:
 GATCCTGGTC CCTCCCTGC TGGACCTGCC ACCCAGAGCT TCCTGNCTAG TCCCACTGGG 60
 CTGGCCACC AGGCCTCTGA CCCAGGCTGC TCTNCGGCC CTTCCTCCTC CTNTTCCTGC 120
 10 TCCAACCTTCT GTCCACCTGG GGACAGTCTG TGCCTGTAGC CTNATGACCC CAACCCAGCC 180
 CCAGGCATGG CTAACCCCTG ACTGNTTGCC TCATATTAA GCTGCTGNTN TGGCCAAGTG 240
 NCTAATTTTA ACCCAGACCT NAATAAGAC ACNTNTTGT ACCAAA 286

SEQ ID NO:7779
 15 SEQUENCE LENGTH:127
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS09029
 SEQUENCE DESCRIPTION:
 20 GATCTGATTT TTCATAAAAA ACATTTGTGA ACCTTCGGCA TAAATGGGTT AAGGTGCCAT 60
 CCCTGAAACT GCAATGCAGA TATGTTCAAG TAACTTTNAT TTNTTAATTA AAAATAAATC 120
 TTTCAAA 127

25 SEQ ID NO:7780
 SEQUENCE LENGTH:105
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS09030
 30 SEQUENCE DESCRIPTION:
 GATCTGANTT TTCATAAAAA ACATAAANTG ACCTTCGGCA TAAATAGGTT AAGAAGCCAT 60
 CCCANAACT NCAATGCAGA TATGTTCAAG TAACTTTTAT TTTTN 105

35 SEQ ID NO:7781
 SEQUENCE LENGTH:321
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS09031
 40 SEQUENCE DESCRIPTION:
 GATCGGCGCC GTTACAGACG TGGCTACTAT GGAAGGCGCC GTGGCCCTCC CCGGAATNCT 60
 GGTGAGATTG GAGAGATGAA GGATGGAGTC CCAGAGGAG CACAANTNNN GGGACCGGTT 120
 CATCGAAATC CAACTTACCG CCCAAGGTAC CGTAGCAGGG GACCTCCTCG CCCACGACCT 180
 45 GCCCCAGCAG TTGGAGAGGC TGAAGATAAA GAAAATCAGC AAGCCACCAG TGGTCCAAAC 240
 CAGCCGTCTG TTCGCCGTGG ATACCGGCGT CCCTACAATT ACCGGCGTCG NCCGNTTCCT 300
 CCTAACGGTN CTTACANGT N 321

50 SEQ ID NO:7782
 SEQUENCE LENGTH:66

55

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09032

SEQUENCE DESCRIPTION:

GATCCACTGA GTTAGTTTCA TTGGGGCGGG GGAAAGAACT GGAATTAAAC TTGTTTAATC 60
CTTAAA 66

SEQ ID NO:7783

SEQUENCE LENGTH:131

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09033

SEQUENCE DESCRIPTION:

GATCCTCCCA GCTGTCGGCC GCGGACCCGG GCCGCGTGTG AGCGGCTTTT GCACCTCCTA 60
TCCCCAGGGT CCGCCGAGAG CCACGATTTT TTTACAGAAA ATNAGCAATA AAGAGATTTT 120
GTACTGTCAA A 131

SEQ ID NO:7784

SEQUENCE LENGTH:143

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09034

SEQUENCE DESCRIPTION:

GATCACAAAT GCATTTTTC A TCTTTACAA TATGAAATNT ATTTATAACT TTAGTTCCAA 60
AATGGACTCT GTAATGCATT TGCCCATATT TTTAGTCGTA ATGGATGTGA TTATATTNA 120
TTGAATTAAA AATCTAACAG AAA 143

SEQ ID NO:7785

SEQUENCE LENGTH:345

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09035

SEQUENCE DESCRIPTION:

GATCTTAACT TTAATAAGGC AAAACAAAAG CTTGAGCTG TTGCGTGTGT AAGTCTGTTG 60
TGTGGATGTN CGTGTNTGGT CCCCAGCCCC AGACTGGATT GGAAAAGTGC ATGGTGGGGG 120
CCTCGGGGCT GTCCCCACGC TGTCCCTTTG CCACAAGTCT GTGGGGCAAG AGGCTGCAAT 180
ATTCCGTCCT GGGTGTCTGG GCTGCTAACC TGGCCTGCTC AGGCTTCCCA CCCTGTGCGG 240
GGCACANCCC CAGGAAGGGA CCCTGGACAC GGCTCCACG TCCAGGNTTA AGGTGGATGC 300
ANTTTCNGNA ACCTCCANTC TTCTGTGTAG CANTTTAAC CNAGN 345

SEQ ID NO:7786

SEQUENCE LENGTH:167

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09036

SEQUENCE DESCRIPTION:

GATCAGCTCT CTGTGAAAAT GGACCAATCA TCAGGATGTG GGTGGGGCCA GATTAGGGAA 60
 TAGAAGCAGG CTGTCTGAGC CAACAGTGTC ANCATGCTTG GGTCCCCTTN CATGCTGTGG 120
 5 AAACTTTGTT CTTTCGCTCT TCACANTAAA TTTGCTGCT GCTCAA 167

SEQ ID NO:7787

SEQUENCE LENGTH:172

SEQUENCE TYPE:nucleic acid

10 TOPOLOGY:linear

CLONE:HUMGS09037

SEQUENCE DESCRIPTION:

GATCCTGGAC AAAGCTTGGC TGCCGGCTTC ATTTATTCCT GCTGATGGCT GAGAAGCATC 60
 15 TGTTTTCCAT CCCACTTGCC TGTCCCAAGT TTTGTTCCAT TTTNAAAAA TTTGTTGTAA 120
 ACTGCATGTT TTATAAATA AAAATAAAAT ATCGTTTGTA ATTTATCTCA AA 172

SEQ ID NO:7788

SEQUENCE LENGTH:255

SEQUENCE TYPE:nucleic acid

20 TOPOLOGY:linear

CLONE:HUMGS09038

SEQUENCE DESCRIPTION:

25 GATCCGCCCC CCTTNGGCCT CCCAACACAA TTTATATTTT TGANGGTCCT TTTATGTGTA 60
 TTGTGCCATA TGCTTCTNAC ATCAGCCCCA ATAAATGCTT TAGGCGTTTT ATATTATCTA 120
 CCACTATTAC ATGCTCTCCA TCTCCAGACT ACCCATTTCT GCCATTGCCC TCATAGGGGC 180
 CCATTCTGAT AATTCTGGAT ATGTAGAAAA ATAAATCCTG TTTATGTGTT TAAATAAATA 240
 30 GATGTATACT ATAAA 255

SEQ ID NO:7789

SEQUENCE LENGTH:256

SEQUENCE TYPE:nucleic acid

35 TOPOLOGY:linear

CLONE:HUMGS09039

SEQUENCE DESCRIPTION:

40 GATCCCTGAC AGCAAAAAGT TTCTTTTCTG AGGCTGCCAT ACTGCCACTG TCCAGGTGGA 60
 GACTGAGCAA AGGAAGTCCT GGGCTGTGCC AGCTCCCAGA GCTTCGGAAG AAAGAGCAGC 120
 AGCTCTCTCC CTGGGAACCA TCAGAGAATT CTGTTGATGT GTTCTGTGTC TGTCTGTCAC 180
 CTGGTCACGA GCTTCTACCA CCTTTGCAAT TGTCATTAT CTTTCACTCC CTGAATAAAG 240
 TATCTATGCA TATAAA 256

SEQ ID NO:7790

SEQUENCE LENGTH:123

SEQUENCE TYPE:nucleic acid

45 TOPOLOGY:linear

CLONE:HUMGS09040

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCTCCAC CTTTCGGGCC ATGTTGCCCC CGTGAGCCAA TCCCTCACCT TCTGAGTACA 60
GAGTGTGGAC TCTGGTGCCT CCAGAGGGGC TCAGGTCACA TAAAACTTG TATATCAACG 120
AAA 123

SEQ ID NO:7791
SEQUENCE LENGTH:310
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

CLONE:HUMGS09041

SEQUENCE DESCRIPTION:

GATCTAGCTT CAGAGGAAGT CTACACCCCA TTCCCTTCTG CTTACAATGT ACCCATGATA 60
TGTGTTTAGC NNNNGAATAC TGTAACAGGA CATCACATGG AAAAATCAAA GCAGCTGGCT 120
CACTGTATTT AACTGAAAAG AATGCCTACA GATTGGATAT TTAATAGGGA AAATTAAGGC 180
ACTTTAATAA CANACTTCAT TATGTGAACT TGTGGAATAT TNNCATAACAN TATACCTTGT 240
ATATTANTGC CATAGTTTTT NGAAACACTA ATTAAACAA CANATTTNAG GGGTGCTGGC 300
ATATCCAGN 310

SEQ ID NO:7792
SEQUENCE LENGTH:61
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

CLONE:HUMGS09042

SEQUENCE DESCRIPTION:

GATCCGAAGG CTGCGGGCAG CGTNTNATCC CGTGGTTTAA TAAAGCTGCC GCGCGCTCAA 60
A 61

SEQ ID NO:7793
SEQUENCE LENGTH:310
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

CLONE:HUMGS09043

SEQUENCE DESCRIPTION:

GATCTTGGTC TTATTTGCAC AGTTTTTGCG TCTTGTTCG TTCTTGCAATC TGATTAACTA 60
GAATATTTCT NTTTCCCCCT TTAAATTTGT GATGTCACCT GACCCCATTT ATGTGTAGGA 120
GCACTACNCC ATTGGTTTCC AATACTGCAC ACATAAGATA CATACTTGTG TGCAGAAAAGT 180
ATCTTCCTCC AGGCTTGTA TACCCTTCAC ATGGAAGATT AATGAGGGAA ATCTTTATAT 240
TCTGTATAAA ANCAAANGCA AATTATATA CTAATATCAT TTGTCTAAAA NTTTAAGTNG 300
TTTTCAAATN 310

SEQ ID NO:7794
SEQUENCE LENGTH:165
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

CLONE:HUMGS09044

SEQUENCE DESCRIPTION:

GATCAGTAGA AAATGGACAT CAAGTTTGAA CAGATAAATC ATGGACAGCC TTATTGTGAT 60
 TGAATGCTT GTAGGTTCTG TGCCAATTTT CCACCACTGT GTACTTTGTT GCTATTAAAA 120
 ACTGTATCAA CTCTAACGGA AGAATAAATT ATTTGTGATT TTAAT 165

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SEQ ID NO:7795

SEQUENCE LENGTH:149

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

10

CLONE:HUMGS09045

SEQUENCE DESCRIPTION:

GATCCGAGAG TNAAGGAAGT TCCCTGTNTT CCCCCTCCTT TTCCACCAGT NTCGCCTCTG 60
 GCCTTCTCTG GCCACTCCTG GGAGGGACTG CCTCACCACC CCTGTCCCGC TGCCAGAAAT 120
 ACACCCACAA TAAAAACCTG AAAACCAAA 149

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SEQ ID NO:7796

SEQUENCE LENGTH:98

SEQUENCE TYPE:nucleic acid

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TOPOLOGY:linear

CLONE:HUMGS09046

SEQUENCE DESCRIPTION:

GATCCAAACT AACTGCCCAA GCACTACACA GCTGGACCCT GNTTCACCT AACCCTCANC 60
 TAGCAATCAA TACAGCTTCA TTATCTGAGT TGCATAAA 98

25

SEQ ID NO:7797

SEQUENCE LENGTH:265

SEQUENCE TYPE:nucleic acid

30

TOPOLOGY:linear

CLONE:HUMGS09047

SEQUENCE DESCRIPTION:

GATCTNTAGC CTCACCCTGN TCTCCTTCCT CCTACTGGCT GCTCAGGTGC TCCTGGTGGA 60
 GGGGAAAAAA AAAGTGAAGA ATGGACTTCA CAGCAAAGTG GTCTCAGNNC AAAAGGNCAC 120
 TCTGGGCAAC ACCCAGATTA AGCAGAAAAG CAGGCCCGGG ANCAANGGCA AGTTTGTAC 180
 CAAAGACCAA GCCAACTGCA GATGGGCTGC TACTGAGCAG GAGGAGGGCA TCTTTCTCAN 240
 GGGNNGGGTG CACTCAATTG GNNNN 265

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SEQ ID NO:7798

SEQUENCE LENGTH:146

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

45

CLONE:HUMGS09048

SEQUENCE DESCRIPTION:

GATCTTACCC GTGCNTGGNC CCCTCCCTC ANAGCCCATG GTAACGAACC CCTAGAAAGG 60
 AGAGAACGGG CGTCAGGGGT GCACAGTCCA CAGCTGAAGA GCAAGGTTT GTGGCAGCAC 120
 GGNCCTGGCC CTCACCCTCT NTNCCN 146

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EP 0 679 716 A1

SEQ ID NO:7799

SEQUENCE LENGTH:317

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09049

SEQUENCE DESCRIPTION:

GATCTCCGGA CCTCGGCTGC AGAGGCCATC GCAGCTTTTN AAAAGTNAAG TGGTTAATTC 60
CCATTGGTGT CTTNCTTAT AGCATTTTCN TCTAACCTAT AACAGGGGG CATTACATTT 120
ANCTTTAGAA CATGTGAATA GGAGGTTTNC TCATGACTTA CCATTCCAGC TGNATGGGAA 180
AGCAAAGCAG AAAACAGTGC CCCAAATGGA AAANAGNTAC TCACACAGAN CAAAACAGTT 240
CTNGGTCTTG TCCTTGGTCT TGTCAAACCT TGCCTGATGC TCTTTCTAAN GTCNAAATAT 300
GANTGATAAG CNGGCN 317

SEQ ID NO:7800

SEQUENCE LENGTH:372

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09050

SEQUENCE DESCRIPTION:

GATCTGGTGA AGTTGTGTAG TAAAGCATTG GGAGGGTCAT TCTTGTCACA AAAGTGCCAC 60
TAAACAGCC TCAGGAGAAT AAATGACTTG CTTTCTAAA TCTCAGGTTT ATCTGGGCTC 120
TATCATATAG ACAGGCTTCT GATAGTTTGC AACTGTAAGC AGAAACCTAC ATATAGTTAA 180
NATCCTGGNC TTTCTTGGTA AACAGATTTT AANTTTCTGA TATAAANCAN GCCNCAGGAG 240
AATTCGGGGA TTNAGGTTT NCNGAATAGC CTATATATGG TGCATCGGNT AGGTCNTTAT 300
TGATTTTTTG ACCCTTTTCG GCTTTACCTN ATGGGAAGAC CCNGTTCNTT TTTAAATNAT 360
CCNGGTTTTT GN 372

SEQ ID NO:7801

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09051

SEQUENCE DESCRIPTION:

GATCAACCTC TGAATTTTAC ATCATGAATG TAATCACCAC TGGAGCTTCA CTGTTACTAA 60
ATTATTAATT TTTGCCTCC AGTGTCTAT CTCTNAGGCT GAGCATTATA AGAAAATNAC 120
CTCTGCTCCT TTTCAATGCA GAAAATTGCC AGGGGCTTAT TTCAGAACAA CTTCCACTTA 180
CTTTCCACTG GCTCTCAAAC TCTCTAACTT ATAAGTNTTG TGAACCCCA CCCAGGCAGT 240
ATCCATGAAA GCACAAGTGA CTAGTCCTAT GATGTACAAA GCCTGTATCT CTGTGATGAT 300
TTCTGTGCTC TTCACTCTTT GCAATTGCTA AATAAAGCAG ATTTTATAAA TACAAA 356

SEQ ID NO:7802

SEQUENCE LENGTH:359

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09052

SEQUENCE DESCRIPTION:

GATCAAGCAG ATTCCACGAA TCCTCGGCCC AGGTTTAAAT AAGGCAGGAA AGTTCCCTTC 60
 CCTGCTCACA CACAACGAAA ACATGGTGGC CAAAGTGGAT GAGGTGAAGT CCACAATCAA 120
 GTTCCAAATG AAGAAGGTGT TATGTCTGGC TGTAGCTGTT GGTCACGTGA AGATGCCNGA 180
 CGATGAGCTT GTGTATAACA TTCACCTGGC TGTCAACTTC TTGGTGTCAT TGCTCAAGAA 240
 AANCTGGCAG ANTGTTCGG GGCCTTATNT TNTCAAGAGC ACCNTGGGGN AAAGCCCCCA 300
 GNGGCCTNTT NTAAGGGCA CCGTTTNGAN NTAAATTTC TNGTTANCCC AGTTCNAAA 359

SEQ ID NO:7803

SEQUENCE LENGTH:134

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09053

SEQUENCE DESCRIPTION:

GATCCGGCCA GTTCATTGAA CAAACCTTTC CTTTTCTAA AGTCCAGAA GCCTTCCTGA 60
 AGGTGAAAAG AGGACACGCA CGAGGAAAGA CTGTAATTAA TGTGTGTTAA ATAAAAATGC 120
 AGTTTAGTGA TAAA 134

SEQ ID NO:7804

SEQUENCE LENGTH:62

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09054

SEQUENCE DESCRIPTION:

GATCTACTGA CATTAGCAC TTTGTACAGT AAAAAATAAA GTCTACATTT GTTAAAAACA 60
 AA 62

SEQ ID NO:7805

SEQUENCE LENGTH:120

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09055

SEQUENCE DESCRIPTION:

GATCTGGATG ATGGTTATGT AGCTGCATAT ATTTGTCAAC ATTCTCATG CTGTATGTTT 60
 AGATTGTGA TTTTACTATA TGTAAATTAA TTCCTTAATA AAATACTATT ATAAAAATAA 120

SEQ ID NO:7806

SEQUENCE LENGTH:209

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09056

SEQUENCE DESCRIPTION:

GATCTAATCT TCTGTGCTCT GTGTATTGGC GACGAGCAGG GTGAGAATAA GTGCGTGCCC 60
 AACAGCAATN AGAGATACTA CGGCTACACT GGGGCTTTCC GGTGCCTGGC TGAGAATGCT 120
 GGAGACGTTG CATTTGTGAA AGATGTCACGT GTCTTGCAGA AACTGATGC CCTCCTGGAA 180

EP 0 679 716 A1

GCCTGTGAAT TCCTCAGGAA GTAAAACCN

209

SEQ ID NO:7807

SEQUENCE LENGTH:59

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09057

SEQUENCE DESCRIPTION:

GATCTTAATT TAAAAATTA AAACCTGGNG TTTTAAAT AAAACCTTT TGTCTTAA 59

SEQ ID NO:7808

SEQUENCE LENGTH:100

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09058

SEQUENCE DESCRIPTION:

GATCAAGTA ATTGCTTAA TGTCTTGTGG AATNAGCTGT CACTTTATAG TTTATGTATT 60
GTGGTGGGTA CCTTAATAAT AAAAGATTT TTAATGTA 100

SEQ ID NO:7809

SEQUENCE LENGTH:118

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09059

SEQUENCE DESCRIPTION:

GATCTGTTTG ATGGTTACAT CAGTGTATAT TTGTCAAAAT TCCTCAAACT GTATGCTTAA 60
GGCTTTGTGC ATTGTATTGC ATGTAAATNA TACTTCAATA AGTACCAAT AGCATAAA 118

SEQ ID NO:7810

SEQUENCE LENGTH:183

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09060

SEQUENCE DESCRIPTION:

GATCCATAAC CTCTTTAGAG ACCGGCTCCT GGATGCAGAA TCCTATGAGG TTCTGGCCAC 60
ACCTGTTTCT TGTCNTCAG GGGCTGACAC CCATGTNCCA TCCCTCTAAA CCCCTGTCCC 120
TAAACCTACC CCATCTNATG TAACTCTGGG GTCCTTGGT CATTAGAGGG TTTNAGGTC 180
AAA 183

SEQ ID NO:7811

SEQUENCE LENGTH:175

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09061

SEQUENCE DESCRIPTION:

EP 0 679 716 A1

GATCTGAATG GTTTTAATAA GTGTCTGGNA ATTCCCCTGC TTGCACTTGT NTNTCTCGCC 60
 CACCACCACG TAAGACGTGC CTGCTTCCCC TTCTGCCATG ATTGTAAGTT TCCTGAGGCG 120
 TCCCCAGCCA TGCAGAACTG TGAGTCAATG AAACCTCTTT TTTTATAAA TTAATA 175

5

SEQ ID NO:7812
 SEQUENCE LENGTH:329
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS09062
 SEQUENCE DESCRIPTION:

10

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GATCCCCAT TCCCCACCCT GGGAGATGAG GGGGTCCCCA TGTGCTTTTC CAGTTCCTCT 60
 GGAATTGGGG GACCNCGCC AAAGACTGAG CCCCCTGTNT CCTCCATCAT TTGGTTTCCT 120
 CTTGGCTTTG GGGATACITC TAAATTTTGG GAGCTCCTCC ATCTCCAATG GCTGGGATTT 180
 GTGGCAGGGA TTCCACTCAG AACCTCTCTG GAATTTGTGC CTGATGTGCC TTCCACTGGA 240
 TTTTGGGGTT CCCAGCACCC CATGTGGATT TTGGGGGGTC CCTTTTGTGT CTCCCCCGCC 300
 ATTCAAGGAC TCCTNTCTTT TTTTCAANN 329

20

SEQ ID NO:7813
 SEQUENCE LENGTH:326
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS09063
 SEQUENCE DESCRIPTION:

25

30

GATCTGCCAG CCCTACATCC GGCCGGGGCC CAGGGAGGGG AGCAAGGAGA AGGCAGGTGC 60
 GCGCANAAGC GGGCCCTGGA GGAAGAGGAG GGTGGCACGG AGGTCTGTGC CAAGAACAAG 120
 CAAAAGAAGC AGCTGAGGAA CCCCCACAAG ACCTTCGACC CCTCTTTGAA GCCAAAATAT 180
 GCAAAGTNTG ACCAGTGTGG AAACCCAAAG GGCAACAGAT GTNTGTTTCAAG CCTGTGCCGN 240
 GGCTGCTGCA NGANGCGNGC CTTCAAAGNG ACTGCAGACT GNCCAGGTNA CGGTTTGCTT 300
 TTTAAACCA ATTTNGGAGA AGTTTN 326

35

SEQ ID NO:7814
 SEQUENCE LENGTH:20
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS09064
 SEQUENCE DESCRIPTION:
 GATCGGAATG NAAATCTAAA

40

20

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SEQ ID NO:7815
 SEQUENCE LENGTH:248
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS09065
 SEQUENCE DESCRIPTION:

50

GATCAATGTT GAAAGTGTG TTATATGGCA AGTNTTTAAC ACATTCACAG TGTTTGTGTTG 60

55

EP 0 679 716 A1

5 ATTTCAACTG TGAATTGTCT TACAGTTTTT TCAAACCTAG TTGTTTCTAT GGACACCTGC 120
 TCTGAATTGT ACATTGACTN CATTACTAAA GAACAAAAAT GTTCATTTTT GTCCCAGTAA 180
 ATTGAGACTG CTTGTACACT TTCAGAAAAA TATGTGAATT TATAAAGNTT TTGTAGATAC 240
 TTGTCAAA 248

10 SEQ ID NO:7816
 SEQUENCE LENGTH:87
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS09066
 SEQUENCE DESCRIPTION:
 GATCCCGGGA TTTNACACTC CTTCTGTTTT GTTGCCGTTT ATTTTGTAC TCAAATCTCT 60
 ACATGGAGAT AATNATTTA AACCAAA 87

20 SEQ ID NO:7817
 SEQUENCE LENGTH:267
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS09067.
 SEQUENCE DESCRIPTION:
 GATCCACCTG NCCCTGACCT CCGACAGTGC TGGGATTACA GGCATAGCCA CCGTGCCTGA 60
 CCAGGGCTCT TTTAGCAAGG AAAACGTGAG GAATGAATGG CTGTTGGTGT GCAACAAATC 120
 ATACTTGCTA CATGTTGTGA ACCTGAAGTT ATTTGTTAGT CTGTATGAAG AATGTACCCC 180
 AGAGATGCAC CCTGTATCTG CCTTATGTCT CTTACAATGG AGGTTCTCTC CTGTTATATT 240
 GCTGAATAAA CTATGTGAAC TGCTAAA 267

30 SEQ ID NO:7818
 SEQUENCE LENGTH:22
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS09068
 SEQUENCE DESCRIPTION:
 GATCTTCAAG CAAGAAAATA AA 22

40 SEQ ID NO:7819
 SEQUENCE LENGTH:90
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS09069
 SEQUENCE DESCRIPTION:
 GATCATAGCT GAAAATTAAT GATACTGTCA ATTTGAGATA GCAGAAGTTT CACACATCAA 60
 AGTAAAAGAT TTGCATATCA TTATACTAAA 90

50 SEQ ID NO:7820
 SEQUENCE LENGTH:25

55

SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS09070
 SEQUENCE DESCRIPTION:
 GATCATTAAA AAATTAATAA AGAAA 25

SEQ ID NO:7821
 SEQUENCE LENGTH:33
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS09071
 SEQUENCE DESCRIPTION:
 GATCCCAATG AAACGAATTC TGTCTCCCTG AAA 33

SEQ ID NO:7822
 SEQUENCE LENGTH:23
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS09072
 SEQUENCE DESCRIPTION:
 GATCTTCAAG CAAGTTAANT AAA 23

SEQ ID NO:7823
 SEQUENCE LENGTH:75
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS09073
 SEQUENCE DESCRIPTION:
 GATCTTCATT TAGCTCCTTT ACTGGGATTT ATTGGATGCT NGTAAAAAAA TAAAATTTAC 60
 ACTGTNTATG CGAAA 75

SEQ ID NO:7824
 SEQUENCE LENGTH:284
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS09074
 SEQUENCE DESCRIPTION:
 GATCAAGAAA GGGCTGTGGC TTGTATCAA GGGTGTTTAA AAGGATTAC TATCAGATTT 60
 GGCCTTGTTT TCTGTGATTT TGGNNAGCGT TCAAGGAAGC CAGGCTTTGG TCTGGATTGG 120
 ATGTTCTCAG GTCATGAATA TAATTCTCTG GGAAGTCCCA AAGTTCTCAT CTACAAAGCA 180
 GAAGTTAATT GGAGCTGAAA ACTAATCAGT AAAGCCACAG CAGCCAGTCA TATGGGGGAG 240
 AAGAGGGGAA TGTGTGATGG TTTTGTGGT TTAGAGGTGA GTTN 284

SEQ ID NO:7825
 SEQUENCE LENGTH:21

EP 0 679 716 A1

SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS09075
 SEQUENCE DESCRIPTION:
 GATCCTTTGT TAACAAATAA A

21

SEQ ID NO:7826
 SEQUENCE LENGTH:159
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS09076
 SEQUENCE DESCRIPTION:

GATCATATTT ATTTTAACTA TTTTITAGA AAATTATTAA TTTTAATTGT ATTTTGTAT 60
 TAAAAAGCT TCTTCACTTG TTTTCCCTAA NNNTTCANAT TGCTGCCCAA AAGTATGACT 120
 GTGGAGGAAA AAAAANTACT TNAANTCC ACACITTTN 159

SEQ ID NO:7827
 SEQUENCE LENGTH:328
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS09077
 SEQUENCE DESCRIPTION:

GATCTGTGCA GGGTATTAAC GTGTCAGGGC TGAGTGTICT GGGATTTC TC TAGAGGCTGG 60
 CAAGAACCCAG TTGTTTGTG TTGCGGGTCT GTCAGGGTGG GAAAGTCCAA GCCGTAGACC 120
 CAGTTTCCTT TCTNAGCTGA TGTCTTGGC CAGAACACCG TGGGCTGTTA CTTCNTTNA 180
 GTTGAAGCG GTTTGCATT ACGCCGTGAA ATGTATTCAN TCTTAANTTA TGTAAGGTNT 240
 TTNTTGTACG CAATCTCGG TTCTTTGANG NGATGGCAAC AAATTTTGGG NTTCTACTGT 300
 TATGTTGGGG NNCATTNGGG CCCANGNN 328

SEQ ID NO:7828
 SEQUENCE LENGTH:108
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS09078
 SEQUENCE DESCRIPTION:

GATCTCCTGA CCTCGTCATC CGCCCGTNTC GGCCTCCCAT AGTGCTGGGN TTACAGGCAT 60
 GAGCCACCAC GCCCGGCTGT TTTATTCTT ATAAGTGTAC AGGANNNN 108

SEQ ID NO:7829
 SEQUENCE LENGTH:277
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS09079
 SEQUENCE DESCRIPTION:

GATCATGAAG CCATCAGCTC CTCTGGGGCC AGCTANAGGA CAACAGAACT NTCACCAAAG 60

EP 0 679 716 A1

5 GACCAGACAC AGTGAGCACC ATGGGACAGT NTCGGTCAGC CAACGCAGAG GATGCTCAGG 120
AATTCANTGA TGTGGNGAGG GCCATTGAGA CCCTCATCAA GAACTTTTAC CAGTACTCCG 180
TGGAGGGTGG GNAGNGACG CTGACCCCTT CTAAGCTACG GGACCNGGGT CACCCAGCAG 240
CTGCCCCATN TTNATGCCGA GCAACTTNTN GNCTGGN 277

10 SEQ ID NO:7830
SEQUENCE LENGTH:123
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS09080
SEQUENCE DESCRIPTION:
15 GATCAGACCA AACAGTGCTG TTTCCCGGGG AGGAAACACT TTTTAATTA CCCTTTTGCA 60
GGCTCCCACC TTTAATCTGT TTTATACCTT GCTTATTAAA TGAGCGACTT AAAATNATTG 120
AAA 123

20 SEQ ID NO:7831
SEQUENCE LENGTH:338
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS09081
SEQUENCE DESCRIPTION:
25 GATCCAGAAA TGGAGACTGG ACCTTCCAGA CCCTGGTGAA TGCTGGAAAC AGTTCCTCGG 60
AGTGGAGAGG TTTACACCTG CCAAGTGGAG CACCCAAGCC TGACGAGCCC TCTNACAGTG 120
GAATGGAGAG CACGGTCTGA ATCTNCACAG AGCAAGATGC TGAGTGGAGT CGGGGGCTTC 180
GTGCTGGGCC TGCTCTTCCT TGGGGCCGGG CTGTTCATCT ACTTCAGGAA TCAGAAAGGA 240
CACTCTGGAC TTCAGCCAAC AGGATTCCTG AGCTGAAAGT AAGATGNCCA CATTCAAGGA 300
30 AGAACCTTCT GCCCCAGCTT TGCAGGATGA ANCACTTN 338

35 SEQ ID NO:7832
SEQUENCE LENGTH:309
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS09082
SEQUENCE DESCRIPTION:
40 GATCTAATCT CAAATACAGT GCTTAGTAAG GGAACCTCTG TGCCTTTGGG GATTTGGGGA 60
TTAAAACGAA TCTTTTAAAT ATATTTCCAA ATATTAAAT ATAAAAGGAT ATTCCTCTG 120
ATGTTAAAAG TGAGTATGGG GGTGGCACAT TATATGGAAA GTNCCATGTT TGCTTAANTG 180
CTATGTAAAA TAACTTGGCA TATTANTGA CTTTGANTGT GAAANTCATA TGCCCTTNGA 240
NTATGGNTGC CTTAGCTCAT TTGACANCTG GNAGANTACT TGTNTATCTN GTTNAGACA 300
45 CATTGANTN 309

50 SEQ ID NO:7833
SEQUENCE LENGTH:233
SEQUENCE TYPE:nucleic acid
TOPOLOGY:linear

55

CLONE:HUMGS09083

SEQUENCE DESCRIPTION:

5 GATCCAAAGT GGCAGGAGGT CTGTGTTGTC ATGGNGAACT GGAGTTTCTC TTGTAAGAGT 60
 TCCCTCATCT GAAATCATGT ATCTNTCTCA CAAATACAAG CATAAGTAGA AGATTGTGTG 120
 AAGACATAGA ACCCTTATAA AGAATTATTA ACCTTTATAA NCATTTAANG TCTTGTNAGC 180
 ACCTGGGAAT TAGTATAATN CCANTGTAA TTTTTNNAT TTACATTTTG TNN 233

SEQ ID NO:7834

10

SEQUENCE LENGTH:99

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09084

15

SEQUENCE DESCRIPTION:

GATCGGAATT TNACAGAATT GGGACTGTGG AACCNNGGGT CACTTGAATT TCCTATATTT 60
 TGTATGGCCA AATCAGGAAC CAGACAGTCT CCATAGTCN 99

SEQ ID NO:7835

20

SEQUENCE LENGTH:288

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09085

25

SEQUENCE DESCRIPTION:

30 GATCAGCCGA TGACAGAGAT TGTAAGCCGT GTGTGGAAGC GAAACTGGNG CCGCCACGTG 60
 CGGGCNCCTGG TGCTTGACCT GTGCTGTAAC GACGAGAGCG GCGAGGATGT CGNGGGGCNA 120
 NAAAANCGGT ACACCATCCG CTGACCCCGT CTGCTCCTCT AGGCTGGCCC CTTGTCCACC 180
 CCTCTCCACA CCCCTTCCAG CCCAGGGTTC CCATTGGCT TCTGGCAGTG GCCCAACTAG 240
 CCAAGTCTGG TGTCCCTCA TNATCCCNCT TACCTGAACC CNTNTTGN 288

SEQ ID NO:7836

35

SEQUENCE LENGTH:32

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09086

SEQUENCE DESCRIPTION:

40 GATCTAAATA AAATGGACNG TTCTACCTTA AA 32

SEQ ID NO:7837

45

SEQUENCE LENGTH:152

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS09087

SEQUENCE DESCRIPTION:

50 GATCTGAAAC AGATGAAAGT TATAATAGTT TACATACCTT ACCTTAAAGT ATGGTTTTTA 60
 AATACTTAAG ATGTGATATG ACATATAGTG TGTATATATA TCTNATNCTA NNGGAAAAAG 120
 GGACATTAAG AAAGCTTATG TAAAAGATA AA 152

55

5 SEQ ID NO:7838
SEQUENCE LENGTH:108
SEQUENCE TYPE:nucleic acid
STRANDEDNESS:single
TOPOLOGY:linear
SEQUENCE DESCRIPTION:
GATCGTTCTT CATGGGGTA AGAAAAGCTG GTCTGGAGTT GCTGAATGTT GCATTAATTG 60
10 TCCTGTTTGC TTGTAGTTGA ATAAAAATAG AAACCTGAAT GAAGGAAA 108

15 SEQ ID NO:7839
SEQUENCE LENGTH:30
SEQUENCE TYPE:nucleic acid
STRANDEDNESS:single
TOPOLOGY:linear
SEQUENCE DESCRIPTION:
TGAAAATTGA TTAACACAGT GTTTTCACCA 30

20 SEQ ID NO:7840
SEQUENCE LENGTH:20
SEQUENCE TYPE:nucleic acid
STRANDEDNESS:single
25 TOPOLOGY:linear
SEQUENCE DESCRIPTION:
TAATACGACT CACTATAGGG 20

30 SEQ ID NO:7841
SEQUENCE LENGTH:25
SEQUENCE TYPE:nucleic acid
35 STRANDEDNESS:single
TOPOLOGY:linear
SEQUENCE DESCRIPTION:
CTTCTTTCTG TAGCCAGGTA ACTCT 25

40 SEQ ID NO:7842
SEQUENCE LENGTH:25
SEQUENCE TYPE:nucleic acid
STRANDEDNESS:single
45 TOPOLOGY:linear
SEQUENCE DESCRIPTION:
TTTTCGGCGC TCCCATTTAT TCCTT 25

50 SEQ ID NO:7843
SEQUENCE LENGTH:35
SEQUENCE TYPE:nucleic acid
STRANDEDNESS:single
TOPOLOGY:linear
55 SEQUENCE DESCRIPTION:
CACGAATTCA CTATCGATTG TGGAACCTTC AGAGG- NH2 35

SEQ ID NO:7844
 SEQUENCE LENGTH:37
 SEQUENCE TYPE:nucleic acid
 STRANDEDNESS:single
 TOPOLOGY:linear
 SEQUENCE DESCRIPTION:
 CTCGCTCGCC CATCCTTATA CAGGCTCAGT TTTGTCT 37

SEQ ID NO:7845
 SEQUENCE LENGTH:37
 SEQUENCE TYPE:nucleic acid
 STRANDEDNESS:single
 TOPOLOGY:linear
 SEQUENCE DESCRIPTION:
 CTCGCTCGCC CATGTATAGG GACAGCATTT CTGAGAG 37

SEQ ID NO:7846
 SEQUENCE LENGTH:38
 SEQUENCE TYPE:nucleic acid
 STRANDEDNESS:single
 TOPOLOGY:linear
 SEQUENCE DESCRIPTION:
 CTGGTTCGGC CCACCTCTGA AGGTTCCAGA ATCGATAG 38

SEQ ID NO:7847
 SEQUENCE LENGTH:22
 SEQUENCE TYPE:nucleic acid
 STRANDEDNESS:single
 TOPOLOGY:linear
 SEQUENCE DESCRIPTION:
 CCAGGGTTTT CCCAGTCACG AC 22

SEQ ID NO:7848
 SEQUENCE LENGTH:22
 SEQUENCE TYPE:nucleic acid
 STRANDEDNESS:single
 TOPOLOGY:linear
 SEQUENCE DESCRIPTION:
 TCACACAGGA AACAGCTATG AC 22

Claims

1. A purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.

2. A DNA probe consisting of a purified single-stranded DNA , a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
3. A DNA primer consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
4. A purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
5. A DNA probe consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
6. A DNA primer consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.

Fig. 1

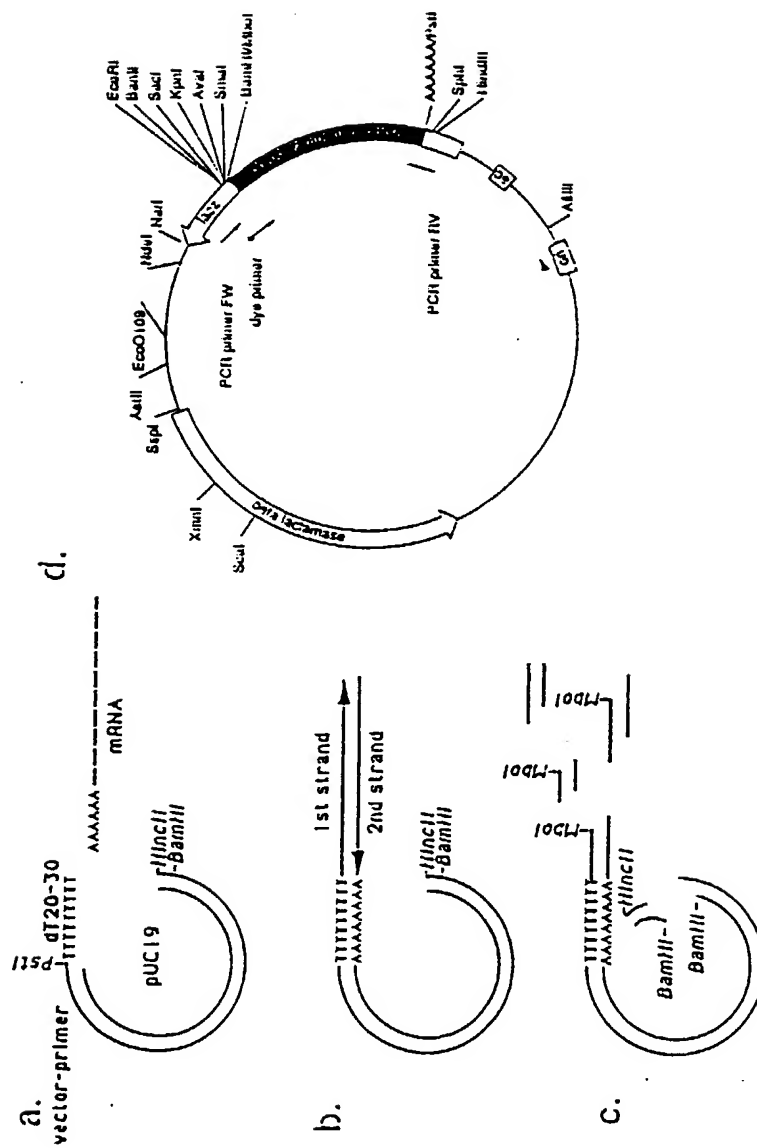


Fig. 2

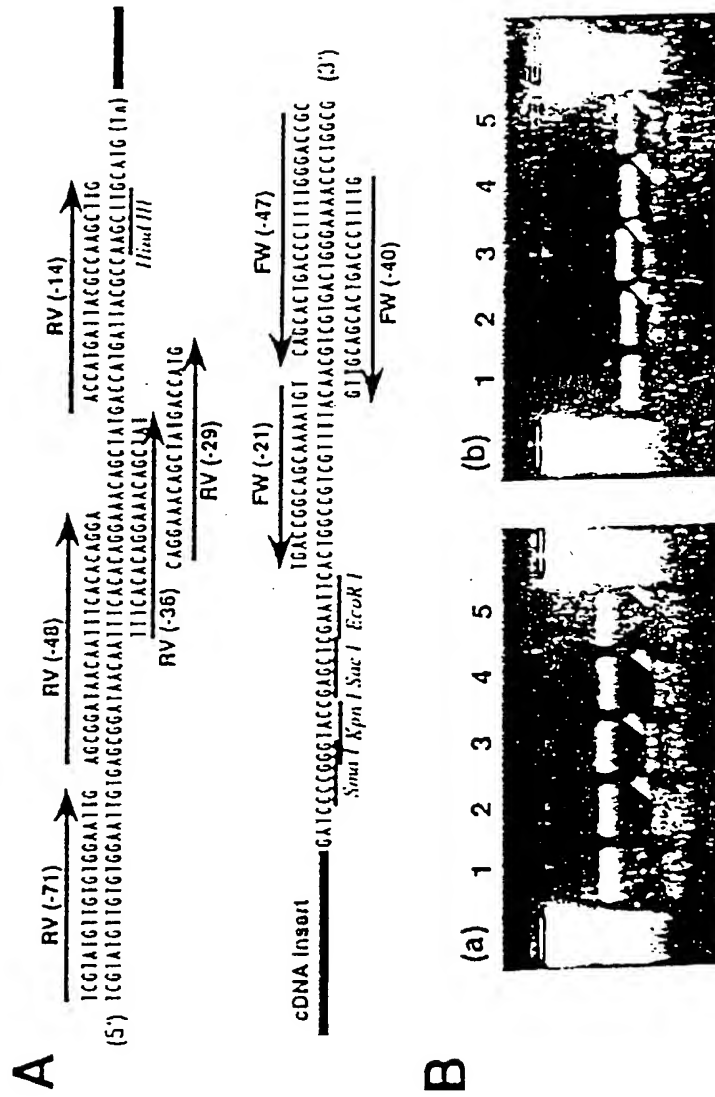


Fig. 3

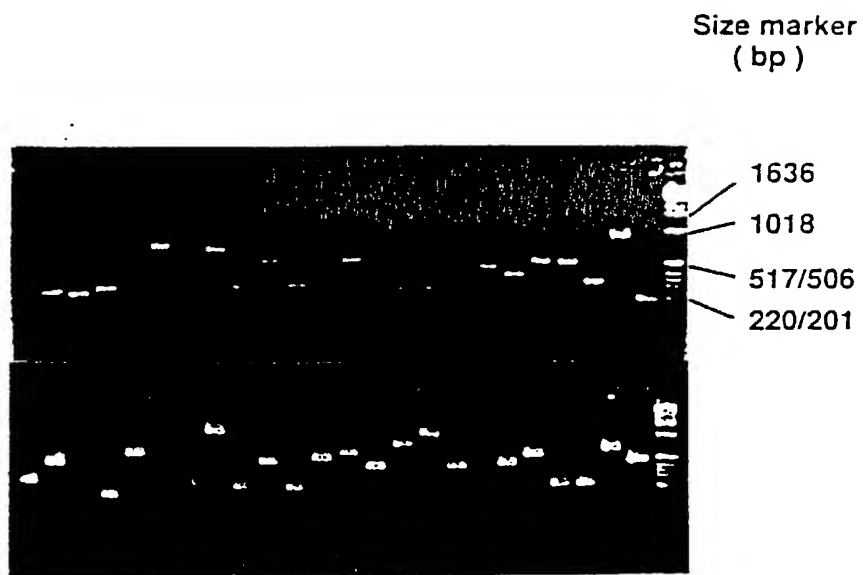


Fig. 4

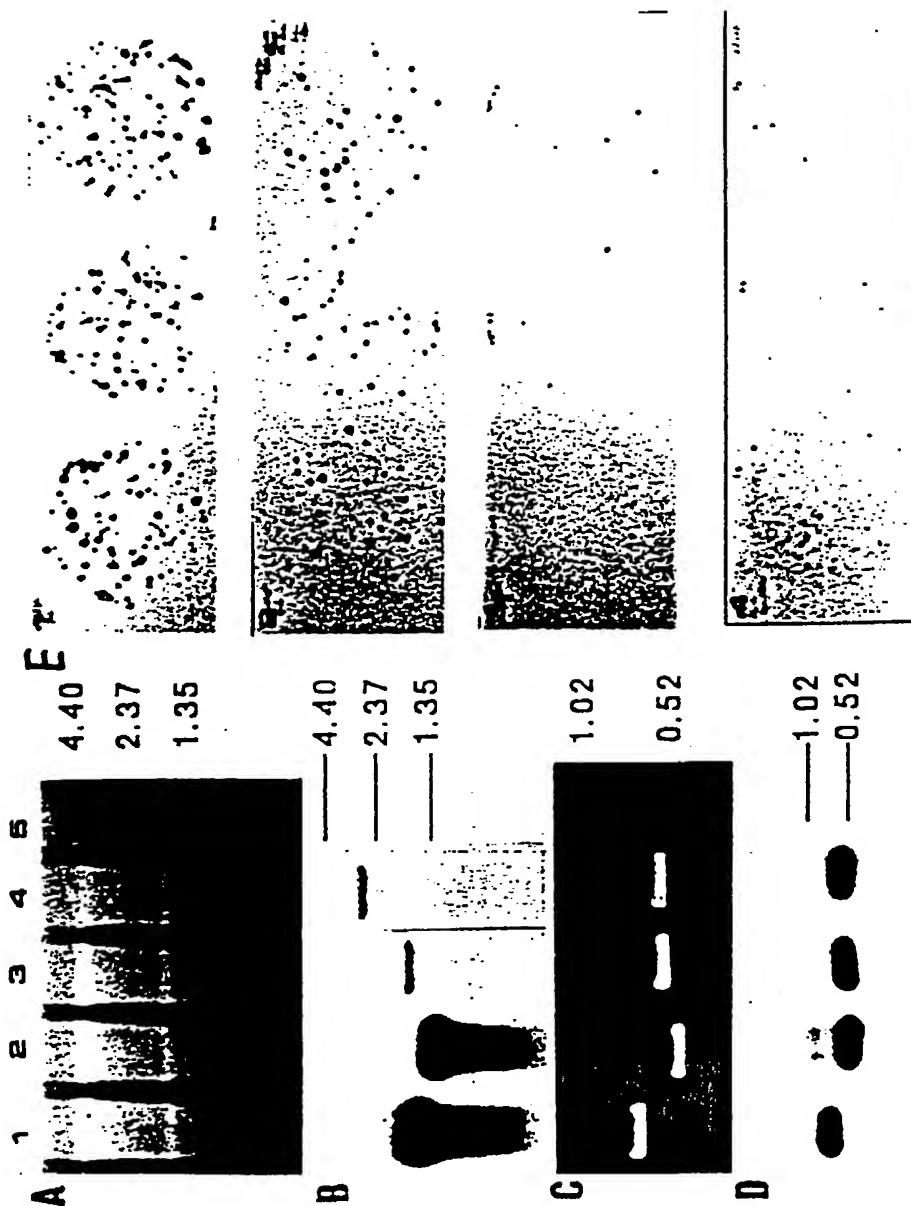


Fig. 4

F

probe No.	1	2	3	4
gene	Elongation factor 1- α	α 1-antitrypsin	HnRNP core protein A1	Inter- α -trypsin inhibitor
(a) Band intensity of Northern blot(cpm)	687	423	10	15
(b) Band intensity of control blot(cpm)	133	177	100	127
(c) Normalized signal(a)/(b) $\times 10$	52	24	1	1.2
(d) Positive signals on colony blot	307	119	7	9
(e) Relative representation	44	17	1	1.3

Fig. 5

Appearance frequencies of various cDNAs in the 3'-directed HepG2 cDNA library					
Group	Clone	Gene	A In 982 (%)	B "in 8,800 (%)"	C "in 26,400 (%)"
I	a15	Elongation factor - 1A α	22 (2.2)	307 (3.5)	NT
	c321	Translationally restricted tumor protein	12 (1.2)	89 (1.0)	NT
	lb030	α -1-antitrypsin	8 (0.8)	119 (1.4)	NT
	hm01b02	Light chain of ferritin	6 (0.6)	62 (0.7)	NT
	c13a04	NADP(H) Menadione oxidoreductase	4 (0.4)	27 (0.3)	NT
	hm02d02	Ribosomal protein S11	3 (0.3)	29 (0.3)	NT
	lb042	Human RNP core protein A1	2 (0.2)	7 (0.1)	NT
	s155	unknown	1	2	5 (0.02)
	s159	unknown	1	2	4 (0.02)
	s639	unknown	1	1	3 (0.01)
II	s635	unknown	1	0	2 (0.01)
	s170	unknown	1	0	1 (0.004)
	s154	unknown	1	0	1 (0.004)
	s167	unknown	1	0	1 (0.004)
	s645	unknown	1	0	1 (0.004)
	s647	unknown	1	0	0 (<0.004)
	s632	unknown	1	0	0 (<0.004)

Fig. 6

Sequences of plasmids										
GS	Chromosomal position	Sense	Anti-sense	AT	IIQ	IIIE	IIIO	CO	Q	T
pml2166	51000784	CAGAGCCCGTACACGAT	AAGTTATGTTGGGTCAG	48	114	115	104	110	1	2
pml2444	91001026	AATGGACAGTTACACTGA	CCAGCTCTGTGACTTGAGA	48	83	81	>200	>200	1	1
pml2883	91001075	TGAGCTGTGATACCTATCT	ACAGTACCCGTGAATGGCT	48	121	124	103	107	4	4
pml1772	91001087	GTACCTGACGCCATAGCAC	ACCATCTCCAGCCACACTT	50	104	104	180	>200	6	6
pml2147	91001094	GCCCTTACACAGAGAACTG	TATTTCCGATCCCGTAAC	51	114	116	>200	200	1	1
pml1771	91001116	GGTTTTCAATAGGTTGTAGACC	GCCCCAATCTGCAAACTG	48	95	95	78	107	1	1
pml609	91001191	TTCGTGATTTGTAACCTTTG	GGCTGAACATTCACCTCTTG	47	97	97	-	200	1	1
pml1351	91001200	TTAAGAAAGCCCTATGGAGACC	AAATCTTGTTAGTCACCTAC	47	97	98	-	-	1	1
pml2982	91001346	TCAGGTCTGCTGGAGGATG	AATCTCACAGCAGATATTG	53	120	122	>200	>200	1	1
pml1518	91001446	AAGGTACAGGATAITTCGAGA	TGCATAGCCCATCTCAT	47	130	125	>200	>200	1	1
pml1439	91001464	CCAAAGCCTCGTTGAACA	TTTGGGAGGCCATAGACAG	51	100	100	>200	-	1	1
pml2427	91001468	TACTCAGTGGAAAGATAAAC	CAGTGGACCACTTTCTTA	40	98	98	-	-	2	2
pml2785	91001521	CCCAATCAAAATGTTAAATG	TTTGAATCAGAGCATGAGTT	43	102,175	100	>200	>200	1	1
pml2291	91001534	CCAGAGATTCAGGGGATTC	GGTACAAATGCAATGACT	46	57	57	78	155	1	1
pml2006	91001572	CCACATGCTCTAGCAGCTG	AAACTTTATGCGAGCTCT	44	58	58	>200	>200	4	4
pml1350	91001606	CATGATACCTTCGGTGGTA	AACAGTAGTCCCGACAT	46	84	108	-	-	1	1
pml1730	91001681	AGCTGAATGTGGCATGCT	CCGTTATTTGCTACATGCT	48	119	110	93	115	1	1
pml2931	91001690	AAAGCAATACAAATACCAA	TTCATATGTTTACCACTA	40	90	90	-	-	1	1
pml2925	91001713	TAATGTACCAAGTGAATAG	TAATGTAATATGCCAGTAA	45	88	88	-	-	1	1
pml2010	91001732	CCAGATGGAAGGGAAAGTCT	CTGGAATAGGAGATCAACAG	47	125	125	150	>200	1	1
pml2935	91001764	TGAGATTTTGTCTCTAATA	GGAAATATCGCTCAGTTG	43	103	103	-	-	1	1
pml2093	91001736	AGTCCCTCTGGCTCTCAT	TATCGTCACTGCCCTTATTG	52	137	137	>200	-	1	1
pml2435	91001742	TTTGTACCTACGTAAAGTACT	ATCCGTGCCACACATAGTA	45	105	108	-	-	1	2
pml1671	91001745	TTATAGGAGTCAATATTTCTGTG	AGTCCCATCTCCACATG	45	87	65	>200	>200	1	2
pml1245	91001745	TTCCTTCGGCTCTAAGT	ATGTACAAATTCGGTATGTAGG	45	75	75	170	190	1	1
pml1246	91001755	ATCTACTGTTGTGAAGTG	ACTGATTTGGTCCCATCTG	44	88	67	-	-	1	1
pml1449	91001755	CGACATTTCACTCTCAT	ATGATTTATTAGCCAGGA	43	88	68	-	-	3	6
pml1758	91001801	TCTGGCTCTTGGGTGGGA	GCCCACTGATACAAATGTC	51	115	115	-	-	1	1
pml1434	91001718	AAAGAAAGCAGACGCTAA	ATGTATAGACAAATCCAAAG	42	90	90	-	-	1	1
pml668	91001218	GTAGTCTCGCCCTTAGC	AAGGATTGATTTCTACAT	43	77	77	-	-	1	1
pml1729	91001277	GGTCTGTTTATTTGACAT	AACAGAGGATGGTTCAGA	43	75	75	155	>200	1	1
pml1822	91001206	GATCCITGGTGTAGTTCAGTC	CTGCMAATACAGGGATCAT	48	83	83	160	140	1	1
pml2209	91001418	ACCCAGTCCCAATCCAGT	ACACTCCCCAGCCCTTACT	55	105	105	113	>200	1	1
pml2455	91001468	ATCTAGCTGGCTGATGAT	TAAAGAGATGAATTTATGCT	42	170	130	190	>200	1	1
pml1252	91002271	GTCCCTTGCATCTGTGTA	AAGCATTTATTTGAGGTTA	43	90	90	95	>200	1	3

Fig. 7

g1000148	4	GGCCAGATTGCTCTAGTAT	GTTCAGTTTATTTCAGAGCA	42	62	62	62	69	1	2
g1001052	4	GTGCCATGCCACTGTGTAT	GTTCATATTCATCATCAA	43	80	80	80	80	1	1
g1001215	4	AGAAATTAATAGCATAGT	TAGAGTCAAGTGTGCTGTG	43	100	100	100	130	1	1
g1001298	4	ATCAAGTTTATTGCTTCA	CATCCATCACATCAAGTC	43	116	116	116	180	1	1
g1000993	5	TCTGTGAAGAGCAGCACA	TCTAAGGAGAGCAGCAGTC	49	101	102	113	200	1	1
g1000694	5	AAGCATGCCATTACACAG	CTAAGAGCTGACCCCTCAT	45	87	87	87	200	1	1
g1001065	5	TACCCACATATTAACAGT	GAGACATAGCAGGTAGAT	44	120	120	120	200	1	1
g1001101	5	TTACCTTACGCTGCTTAC	AGACAAATATCCAAAGC	47	89	89	100	200	1	1
g1001161	5	ATTTGTAGGTGTTAGTA	AGAAATGATGCTTTATTC	43	101	99	99	200	1	1
g1000053	6	TGCTATAGTCTCTTCCA	TGCTATGATGCTCTTCT	44	78	78	72	200	2	3
g1001326	6	CATTGACACAGCAGCAG	CCTGCCCTCTCTCTAGTA	53	102	104	145	200	1	1
g1001434	6	TAGGCAAAACAGAGAGAG	AAGAGAGTGGTGCAGGTC	48	65	65	110	200	1	1
g1001457	6	TATATGCAATATCCAAATCTG	TCTATATTTGCTGCCCTATCT	46	90	90	200	200	1	1
g1001523	6	TTGTAAAGTGTGCTCAGT	TTTAAATGTCATGTTAT	42	86	70	200	100	1	1
g1001525	6	GGACCTAAGCCTCCCAAGT	TTTATATCAGTCCAGAGC	48	138	138	200	200	1	1
g1001562	6	TCTGTGATGAGCAAGGAC	TTTATATGATGATCATTC	43	62	62	200	45	1	1
g1000674	7	GACCTGAGTGTGAATGAGT	AATTAGCTTATGGGATTT	45	119	119	200	1	2	
g1001145	7	AGCCAACTCGGGGTCTCT	CCAGGGACAGGTGATCAT	56	159	159	115	200	4	4
g1001469	7	AATCATTTGGCGAGAGTGA	AAGACAGCTTATCCAGACA	45	88	89	130	1	1	1
g1001579	7	TCAGGAGTCTGCTCAGATA	TTGCGAGTTAATCTGTTA	44	77	78	170	1	1	1
g1001207	8	AACAGTATTTGGTTGTGAC	TCCATTAAAGGCCAGTCTCAG	47	81	81	105	70	1	1
g1001176	8	TTGCTCTAATGGTGTCTAC	AAAACCAACACACTAAG	48	99	99	118	180	1	1
g1001248	8	TGTATTGATTTGGATTCTC	CAAAAGCAAAACAGCAGATA	44	95	95	85	1	1	1
g1000260	8	TTGCCATCAAAACATACA	CTGTGAGTTTGGTTCTG	43	55	55	1	1	1	1
g1001055	9	TTAAGATACCCCTCATTC	CACATGCTTATGGACACT	44	74	74	72	73	1	1
g1001157	10	AAGTATTGTGCAAAAGATGA	AAGAAACAGCTGCTGTG	45	138	139	200	200	2	3
g1001284	10	TGTAAATGCTATCTCTCT	GCATGCTTCCATATCAGT	47	100	100	200	200	1	1
g1000224	11	ATCAAAACAAACATCCAGA	ACTATAATATCTGCCAAGT	42	117	121	134	95	2	2
g1001169	11	GAATAGCTGGAGATTTCAC	GGAGATCATACCTTCAGCA	46	100	100	84	95	1	1
g1001315	11	AAAGTGACCTTGATGGACAGTGA	TGAGCCCAAAATACATGCTGACT	50	153	153	200	160	1	2
g1001352	11	AGGCTGAAGGTTATTTACG	CACATGCTTGAGAGCTA	47	83	85	1	1	2	2
g1001489	11	AAGCTCTAGTAAAGCATTC	TTATTAAGCAATCCAGTA	37	47	47	125	53	1	1
g1001570	11	CTGTAAAGGTTTGGAAATATGT	TTTCATTTTCTACCATTTAT	42	75	75	145	200	3	3
g1002279	12	AGTGTATGAGACCTTGAG	GTTCATGAAAGGCTGAGC	48	130	130	103	200	1	2
g1001163	12	TCTCCCTATTCACACCAGT	AATGATTCTGAGGATAGCA	49	88	88	200	170	1	2
g1001193	12	CACAGCATAAAGATCATTA	ACCTAATTTAGTTTCTCAC	46	100	100	100	1	1	1
g1001235	12	CATCATGGTACAGTCAGAG	CAGTTTGTCAAAATGTATG	44	83	82	83	87	1	1
g1001274	12	AGATGTCAGTATCTCTCTAG	GAGAACAGCAGTAAGCAGCAC	47	87	87	200	200	1	1
g1001308	12	CCAAAGTGTAGGTTTACAG	TTCAATAGACCTTGGTTAC	47	95	95	200	200	1	1
g1000153	13	CTAAGATTATATGCGATTC	AGTAGTGTATGGCAGAGTA	46	104	104	200	200	1	2

Fig. 8

91001044	pm1558	13	TTTAAAGCTATCAGAGTCA	AGACAGACTATGCCATCTA	44	108,200	109	>200	100	1	1
91001200	pm1721	13	GCTTCTGCTGCTGCTGGT	GCAGTATCATGGCTATTCTCC	50	122	122	>200	190	1	1
91001362	pm0116	13	ACTGAAATGGAACATAGTCT	TACATTACATGACATTGTGA	40	61	61	95	103	1	1
91001366	pm0364	13	TGCTTAGCTTCCCTCCTTA	GAGCATTTGCTGTGCTGA	45	67	67	-	-	1	1
91001389	pm2301	13	CATGAACCTGCTCAGGACA	GCCTTACTTATGCTGACC	51	100	100	100, >200	-	1	1
91001492	pm0541	13	AAATGAATGTAATAGCACT	ATTATTTTACAGGGAGAT	41	72	72	-	74	1	1
91001367	pm0441	14	GTTTATGTTTGAATTTGGG	CATTCACCTTACATTCT	42	77	77	>200	180	3	4
91001584	pm2307	14	CGTTCTAACTCTGAATTC	AATGCTATTATTCGAAG	42	55	55	>200	>200	1	1
91001576	pm2019	14	ATCACAATACCTTTAGTTG	ACGATACCTTATGGAGAT	39	69	69	-	-	1	1
91001339	pm2220	15	TCCCATCTCAGTTGAGT	TGAGACAAAAGAACCACT	47	70	70	80	150	1	1
91000980	pm0985	16	TTGGAATGAACCTTGCTA	ACTATGCTGCTGAATGG	48	79	79	68	70	2	2
91001242	pm1127	16	CCCTGTTTTACATGTTCA	TATTAATCTCCCATCAT	44	105	105	103	102	2	2
91001516	pm2543	16	ACAGTCTAAATCAAGGTG	TGTGCACTCAAGGTGCAAT	45	70	70	>200	-	1	1
91001566	pm0912	16	TTTGTGGGACTATGTAA	TGACTTTTATGGGAACCA	41	53	53	>200	>200	1	1
91000906	pm1157	17	CTCTCATGTTCTGTACAA	TAGAAGGAATCTGTGGT	47	77	77	140	>200	2	3
91001015	pm2368	17	ATATTCACCTCCCATCCAT	TCAATACGTCCTCTCAGC	50	80	80	>200	>200	1	1
91001156	pm2202	17	CAGAAATTAAGTGCAGCAAT	TGATCTGCATCTTAAAT	45	103	100	>200	>200	2	2
91001173	pm2117	17	AAATCTGTGGTTATTTCC	TGATGCTGCTGACATTGC	41	118	118	145	200	1	1
91001201	pm1076	17	TAAATTTGGAAATCTTTGGA	ACACATTTGGGTTGCTTAA	47	100	100	95	97	1	1
91001316	pm0514	17	TGTGACAGCAGCAGCTTCAT	TGCTACATTTTATTCACCC	45	128	129	-	1	1	1
91001356	pm0538	17	CATCTCAGACACAGGAAAC	ACCTAAGATCCAGAGAAAC	40	90	90	69	>200	1	1
91001212	pm2212	17	TGACTGCAATAGGAGTTGT	GACATACACAGTTTATTTCT	46	90	90	180	>200	1	1
91001522	pm0642	17	GTCTCAGCAGATTCAGGT	ACTTCTCTCTGAGGACACA	45	68	68	160	-	1	1
91001076	pm1015	19	TGTGTTCTCCAGCTTTGTAG	GTTACATTTGCTTGGTACAG	48	65	65	>200	>200	1	1
91001417	pm2289	19	GGATCAGACACACAGTGTCT	GCAGGTATTAACAGATTA	46	50	50	-	-	1	1
91001467	pm1688	19	GAAACCCAGCTGCACCTCA	GGAGAGTATGGGAAACGGT	54	93	93	>200	>200	2	2
91001069	pm1079	20	GCCATGCTTGTAAAGTATGT	TTAAGAACCCATTAGTAGATA	48	140	140	-	-	1	1
91001146	pm1146	20	GCCCTTAGGATTCAGTCTC	ACCACCCAGGCTTTTCAGG	52	66	66	180	>200	1	1
91001128	pm0112	20	TGCTGGATGACTCTACAGC	TCCCTATCATGGCTGCTGTT	49	59	59	59, 115	59	1	1
91001132	pm0647	20	CTGCTGGCTAGTCTGACTC	CAATGGTCTAGAGGACAT	49	135	135	153	160	1	1
91001158	pm1774	20	TCTGATGATGATGGAAACA	ATCCTAGTCCCAACCCAGTA	48	109	109	-	-	1	1
91001210	pm1235	20	AGCCATCTGGTTATGTCTTA	AAATGTACCCCTGGCACCTC	52	124	124	>200	>200	1	1
91001377	pm1701	20	TCCATGTGTTAGAAAGCCAG	GGAGCAGATGAACCTTCAC	44	90	90	>200	>200	1	1
91001395	pm2101	21	GTGAGCTCAATGCTACAG	CCACATCTCCACAGGGAGT	54	142	142	>200	74	1	1
91001427	pm0648	21	CTCTGCTATAAAGTAGAG	TTTATAGTGCACACAGAGT	45	130	130	180	>200	1	2
91000978	pm0912	22	GGTGTAGTGAACCAATTAG	ACAAATGGTTCATTAATGA	39	58	58	145	>200	1	1
91001444	pm0911	22	GGTCTTTGTTCTCCCATCTGT	AGTTGCACCCATCTCCTGTC	46	124	124	>200	>200	1	1
91001473	pm2231	22	TGAGTGTACATTAAGTGAAG	AGAAAGCCCAAGTAGTCC	48	65, 88	65	100	175	1	2
91001479	pm2228	22	TACAGCCCTCCCAAGCTAAC	AAGCAGTTGAGTTGGGTTTTC	50	94	94	67	135	2	4
				TTTATCTGCATCCCATACAA	46	65	65	190	>200	1	1

Fig. 9

91000999	X	CTGCCATAGTACCTGGATT	TCACCCACCAGTATTAGCA	47	103	-	-	1	1
91001119	X	GGAGGGAGATACGATTGT	AAAAATCCAGAGCTGA	46	70	70	135	150	1
91001161	X	TTCTATAGTGTACCAGTT	GTAGGATTGAGATACACA	40	85	85	>200	77	1
91001406	X	TAATCCAGTGAATGTTCGTAA	GTAAAGTTATCTTCGATCAGA	47	82	82	>200	80	2
91001168	1,18	ATCCTGCTGAAATACATCTG	GGGAGAGACATACATGAC	46	70	70	68	130	1
91001436	1,2,12,13,Y	TTGCAATGGAGGTGAAT	AATACAAAGTAAACACAA	44	69	69	170	-	1
91001404	1,2,3,5,8,12,14,17,X	TTGGAATGACATCTCTAT	TTTATGTACAAAGCACT	43	130	130	150	132	2
91002803	1,2,3,5,8,12,14,17,X	TATCAAGGTGAAATGTCAC	TTACTGAATCCAGCCAGCA	45	93	93	110	-	1
91000110	1,2,8,X	TCCAAATGAGAGGTGTTA	AGTTCAGACCCAGGTGAATG	43	98	98	100	100	1
91001351	1,3,4,5,8,16	GTCGTGACGCAAGATTC	TTATATGTTGTACAGTCG	43	61	61	-	-	2
91000326	2,20,21,22	GTCGTGACGCAAGATTC	ATCCCTTCTCTCCAGTTA	46	82	82	>200	82	1
91001077	2,4,5,10,12,15,17,20,22,Y	GCCTGTATTTCCACCTC	CAGTCAAAACACACGGTAT	49	95	95	83	160	1
91001192	2,5,14,C	TCTGAGGACATCCAGACAG	CCGTTGAGGTGATGAATG	49	78	80	>200	>200	1
91000213	2,8,12	TGCATTAAGGGAAGACCA	GCAGTACAAATCCCAACT	50	133	133	>200	150	2
91000919	2,8,12,17,X	GTCAATGTATGCAATTTCC	GATTTAACCAATAGGAAGC	50	101	101	101	88	3
91001109	20,X	CATGTACTCAGAGCACTTC	ATAGTATGGGTGACACAGTA	43	80	80	>200	120	1
91001426	3,6	CAGGAGTGGAGCAGGAAG	ACAGCTCAGGAGATGTAC	47	93	93	95	>200	1
91001391	3,4,M	TGGAATTCCTTACCTTGT	GCCTTACACCAACAGCAG	50	96	96	>200	175	2
91000077	3,8,10,15	GCATACAGCCAAATCAGA	GTATTATGTACGGCATTTAC	44	105	100	>200	>200	2
91000605	4,6	GGATTCTATTGCTGTGAT	CTGTCCATGTGGCATAAACC	44	110	110	105	107	1
91001212	6,20	GCATTAAACAGGAACAATA	TTTAGACATACAGAGGAGT	43	81	81	102	-	1
91001312	7,18	AGATGCTACATTAGGGATA	CCCTTACCCCAACACTCTT	55	75,130	75	>200	>200	1
91001441	9,11	CCAGACTACAGGCTGTGGC	CCCATANTAGTGAAGAGTACTTC	48	125,155	127	125	>200	1
91001357	9,14	ACCANTGTACGCTCTAAATA	TTATCTGACTGGAGGAAAT	42	107	107	-	-	1
91001357	10,15,22	AAGAAATGTTTACTGGATT	TTCATTATTGATTAGTTGA	46	100	100	170	-	1
91001261	10,15,22	ACTACCCCTGAGATATTAGTT	CAGGAGGCTACTGGTCTT	50	72	74	72	>200	3
91001456	11,M	ATACCAGTCCCGCTGTCCAG	TTGGGAATGAGAAATAACT	48	83	83	81	-	1
91000290	12,19	GCACCAAGAGGAGTTCAG	TACATACAAAGATGCCAAACAGT	44	80	80	79	68	1
91000103	12,M	GATCAGTCTGCGTTTAT	GTCTCTCTCTGATGCTGA	46	62	60	135	180	1
91001487	13,16	ATCTGTGTGCTGCTTCC	AGGTATTTGTCACACAGAA	48	87	87	>200	>200	1
91002780	14,16	AACCTGTTTACCAGTCTT	AGAACACATCAAAAGATGC	46	90	90	>200	90	1
91001435	17,20,C	TGTTGGTTCACCATGAGAC	CTAGTTATTCCTGCTCTG	44	81	81	>200	200	1
91001393	17,22,Y	GAATGTCATCCAGACGTAG	TCTCTCTCTCTCTCTCTC	49	120	120	>200	170	4
91000056	17,C	TTTATCCAGGACAGCAAC	TGCTCTCTCTCTCTCTCTC	43	95	95	>200	95	1
91001369	17,C	ACTTAAAGTACGTTGTACG	TGCTCTCTCTCTCTCTCTC	44	92	92	-	92	1
91001410	18,C	CCCAGGTTAAAGATATTGT	CGTAGGTCATCTCTCTCTC	46	75	72	160	65	1
91001217	19,20	TGCAGAGTGAATTTCCAGAG	GCCTGTTTACTCAGTCTAC	46	110	110	130	170	2
91001009	19,22	ATCCCTGCTCTATTCACAC	AACCTCTGGGAACAATCAT	48	91	89	160	86	1
91001172	19,22	GCCTGCTCTGTGTTGACTT							

Fig. 10

91001057	pm12049	C	AGGACACAAACCCAGCTAT	TTTCTGATTATGACATGAC	45	75	75	101	75	1	1
91001073	pm1753	M	ATCTCTTTGATGCGATCTG	GTTAAGTGTGATGCCATT	42	54,100	64	64	>200	1	1
91001096	pm1236	M	GTAGAGCTGCTATGATGACC	ACAGACAAAGGAATATCAT	42	108,96	110	110	112	1	1
91001166	pm1508	N	GTCCACAGTCCAGCCTAAC	GCCACATATAGATCCATC	46	74	74	74	>200	1	1
91001151	pm12354	M	TGTCTTTGAGAGCTCTGCGT	TTTAAACAGTCAATAATACATGTT	44	110	110	110	106	1	1
91002029	pm2402	M1C	GCTAGAAAGAGGGGCACTCA	CTTAACCTGATGCCAGGTC	46	75	75	75	75	1	1
91002073	pm2786	M1C	CACAAAAGAGCAAACTTCAG	ATGGTTATTTATCAGATTG	41	83	83	82	83	2	3
91002074	pm1704	M1C	TCCACCCAGAGAACGACACT	AATCATAGGGAATAGGTTG	40	75,130	75	75	75	1	23
91002075	pm1689	M1C	TCCACCCAGAGAACGACACT	GAACAGGTTAGTCCATTCG	48	58	58	58	58	1	1
91002075	pm1442	M1C	CATGAGGCTACGGAACAGG	ADGAGTCCGTGGCTTTCAG	51	81	84	84	81	4	18
91002075	pm1452	M1C	AAAGCATCTTGAGAGGAACA	GGAGGACTCGCTGGTCTTA	49	110, >200	110	110	110	1	9
91002075	pm1452	M1C	GCACAGATACCTTTACACC	TGGTTCTATTTCAGTTCCTTC	51	102	105	102	102	3	13
91002095	pm2268	M1C	GAAGCTCTTGAGGAAAGT	CAGACCCCATCTTTATACC	47	70	70	70	78	3	4
91001018	pm2783	M1C	ACGATATTATAGTGTG	TCAAACTTAAATATAGCT	40	93	93	91	92	1	1
91001053	pm1144	M1C	AGATGAGTGTGGTTCAGAGA	CCATTCTTCATTCAGATT	52	135	140	135	135	1	1
91001127	pm12290	M1C	ACTGGTGATGGAAGGTTACA	CCACAGGTGAGCACCGTCT	47	55	55	55	55	1	1
91001167	pm1626	M1C	GAGAGCCCTGCATCCCTTA	CTCCCTTTGGTCTTCTGT	48	100	100	100	100	1	1
91001216	pm12109	M1C	TAGTCAGAGATTTCAGTAAGT	ACATGTATTTTGATATCTT	42	110	110	110	110	1	2
91001253	pm1240	M1C	AACTGGTTCATCAAGACTG	AGTGAATAAAGTCCCACTCC	48	120	120	120	120	1	1
91001281	pm11131	M1C	ACTTAAAGACCCAGCAGCAT	ACAAAGCAGTCAATAGAA	47	97	97	97	97	1	1
91001375	pm10952	M1C	AAGAGGAGTTCCCTGCTCA	ATGAGCAGATGGCAAGGA	51	89	89	89	150	1	1
91001386	pm2216	M1C	ATCTGATGAGCTATATCT	CGTCTCTTTTATTCACAT	45	108	108	108	108	1	1
91001411	pm10958	M1C	ATGGGTTATCAGGGGTTTC	GAGACCAAGGCACTCTTA	47	89	77	89	80	1	1
91001460	pm2626	M1C	ACATTGATGGGATGAGGT	GGACATTCAGCCACAGC	51	75,55	75	75	75	1	2
91001482	pm1210	M1C	TTGTGACATTCCTTTTAGAA	CAGTGCCTCTGATGAGACA	48	85	85	85	85	1	2
91001490	pm10109	M1C	GCCCACAGAGACATCATCT	TCTTAGAGTGGCTCTGGTG	51	98	98	98	98	1	1
91001618	pm2042	No product	CACCCAGTTAGGCTGAAAGT	GAATAATCTCTGATCATCA	45	87	87	87	87	1	1
91001650	pm1304	No product	CTTTGGGATATTTTCTCAT	CCCTCGGCTAGTTCCTATG	43	60	60	62	62	1	2
91001683	pm1808	No product	AGCCAGCCTCTTTGATGTC	CTGGATTGATTTTCATTAG	44	87	87	87	112	1	1
91001754	pm1673	No product	TGTGGTATGAAATATCTGA	TTATGATGAGACAAACAT	43	98	98	183	>200	1	1
91001765	pm2008	No product	CAGTAGTGTGCTTTGAAATG	TTTAGTGAAATGTGGTGT	41	63	63	63	150	3	3
91001773	pm1761	No product	TACAGCCCTCTTAAAGTGC	TTTGAGCCTCAAGGAAATCT	48	82	82	82	>200	1	1
91001556	pm149	No product	TACATCTTCAGACTCATCG	TTTCAAAAATTTATCTT	40	86	86	86	>200	1	1
91001574	pm1784	No product	ATCAGAGCTCAGTTCCTGTAG	ATTTCCTCTTCGATGGTC	44	57	57	67	67	2	2
91001622	pm1606	No product	GATCTGAGGCTTAAGTGA	TTTGCAGTTCAGCTTATTC	45	54	54	54	54	1	1
91001640	pm1852	No product	GATCTCTCTCTCTTTTCA	TTTATACAAAGACCATAC	38	45	45	45	45	1	1

Fig. 11

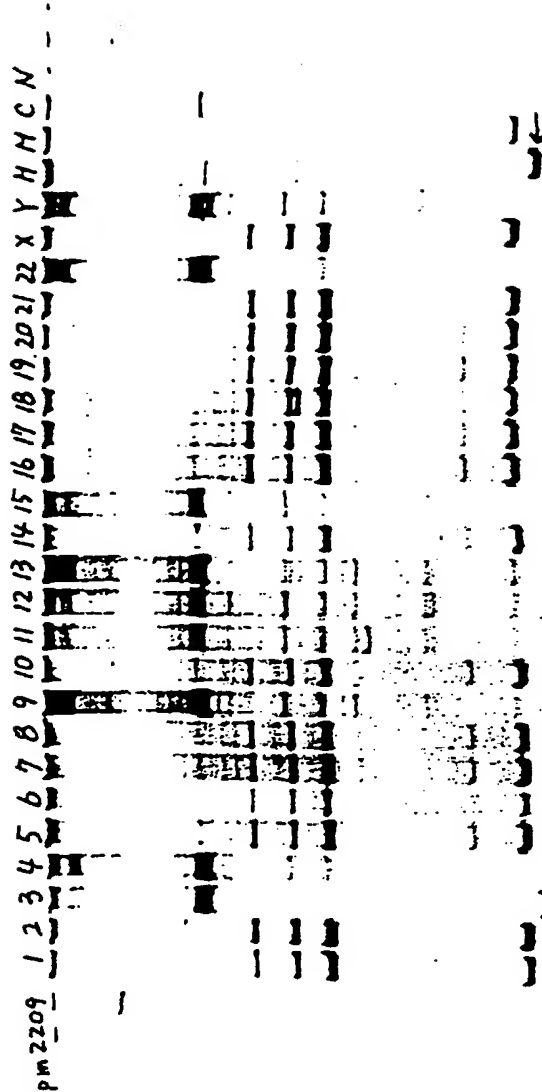


Fig. 12



Fig. 13

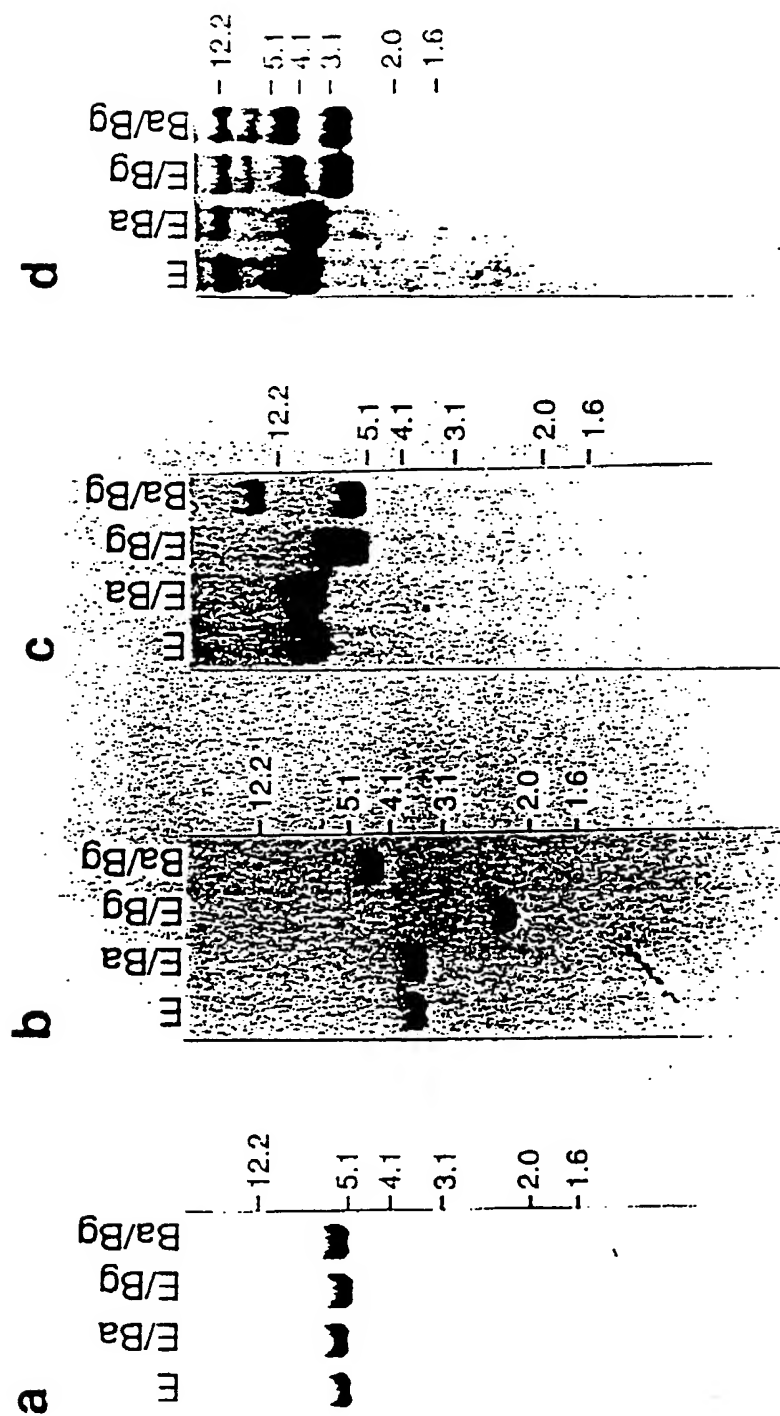


Fig. 14

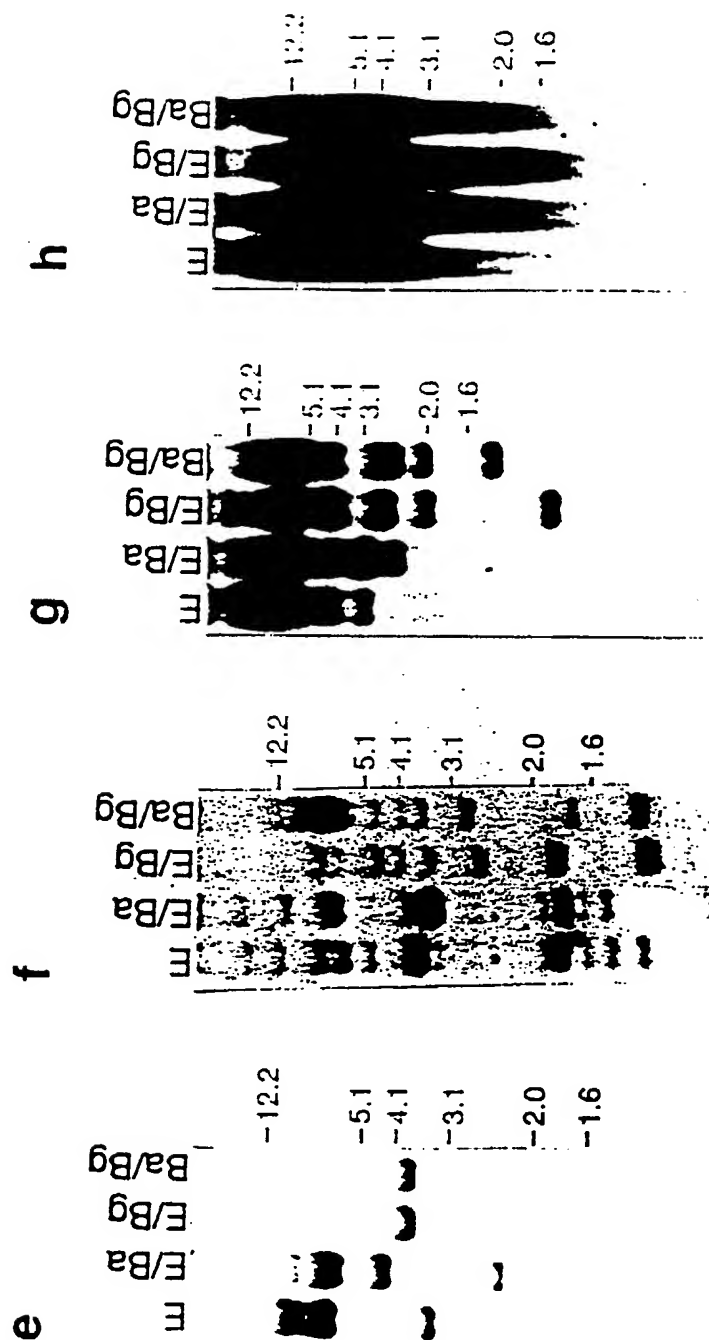
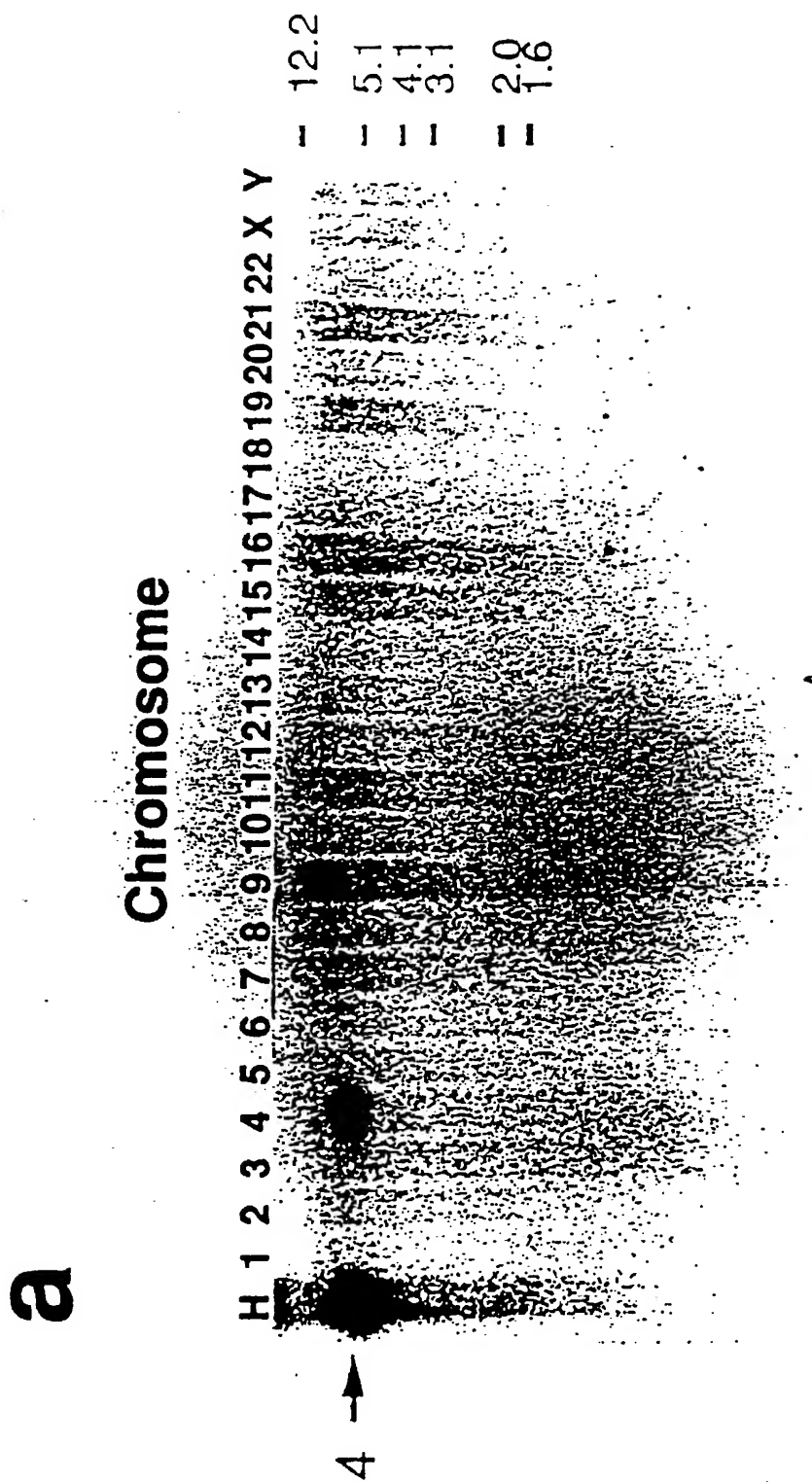


Fig. 15

Hybrid cells used for Southern hybridization

Hybrid cell	Human chromosome	Parent cell No.	Intact chromosome (%)	Translocated chromosome (%)
A9(neo-1)-4	1	A9	100 (0)	0
A9(neo-2)-1	2	A9	93 (8)	0
GM10253	3	CHO	100 (0)	0
GM10115	4	CHO	100 (0)	0
A9(neo-5)-4	5	A9	40 (0)	90
A9(neo-6)-3	6	A9	100 (60)	0
A9(neo-7)-2	7	A9	100 (89)	0
A9(neo-8)-1	8	A9	91 (82)	0
GM10611	9	CHO	79 (5)	11
A9(neo-10)-3	10	A9	94 (6)	75
A9(neo-11)-1	11	A9	24 (0)	76
GM10927A	11	CHO	96 (21)	4
A9(neo-12)-4	12	A9	0 (0)	100
GM10868	12	CHO	82 (6)	0
GM10898	13	CHO	82 (0)	10
GM10479	14	3T6	76 (29)	0
A9(neo-15)-2	15	A9	9 (0)	78
GM11418	15	CHO	62 (0)	100
GM10567	16	A9	69 (0)	0
GM10498	17	LTMK	80 (10)	0
A9(neo-18)-5	18	A9	100 (66)	0
A9(neo-19)-1	19	A9	92 (23)	8
A9(neo-20)-3	20	A9	81 (5)	17
GM08854	21	A9	81 (24)	0
GM10027	22	CHO	93 (0)	100
GM10324	X	A9	81 (10)	0
GM06317	Y	CHW1103	91 (0)	9

Fig. 16



b

Chromosome

H 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y

12 →

- 12.2
- 5.1
- 4.1
- 3.1
- 2.0
- 1.6
- 1.0

Fig. 17

Fig. 18

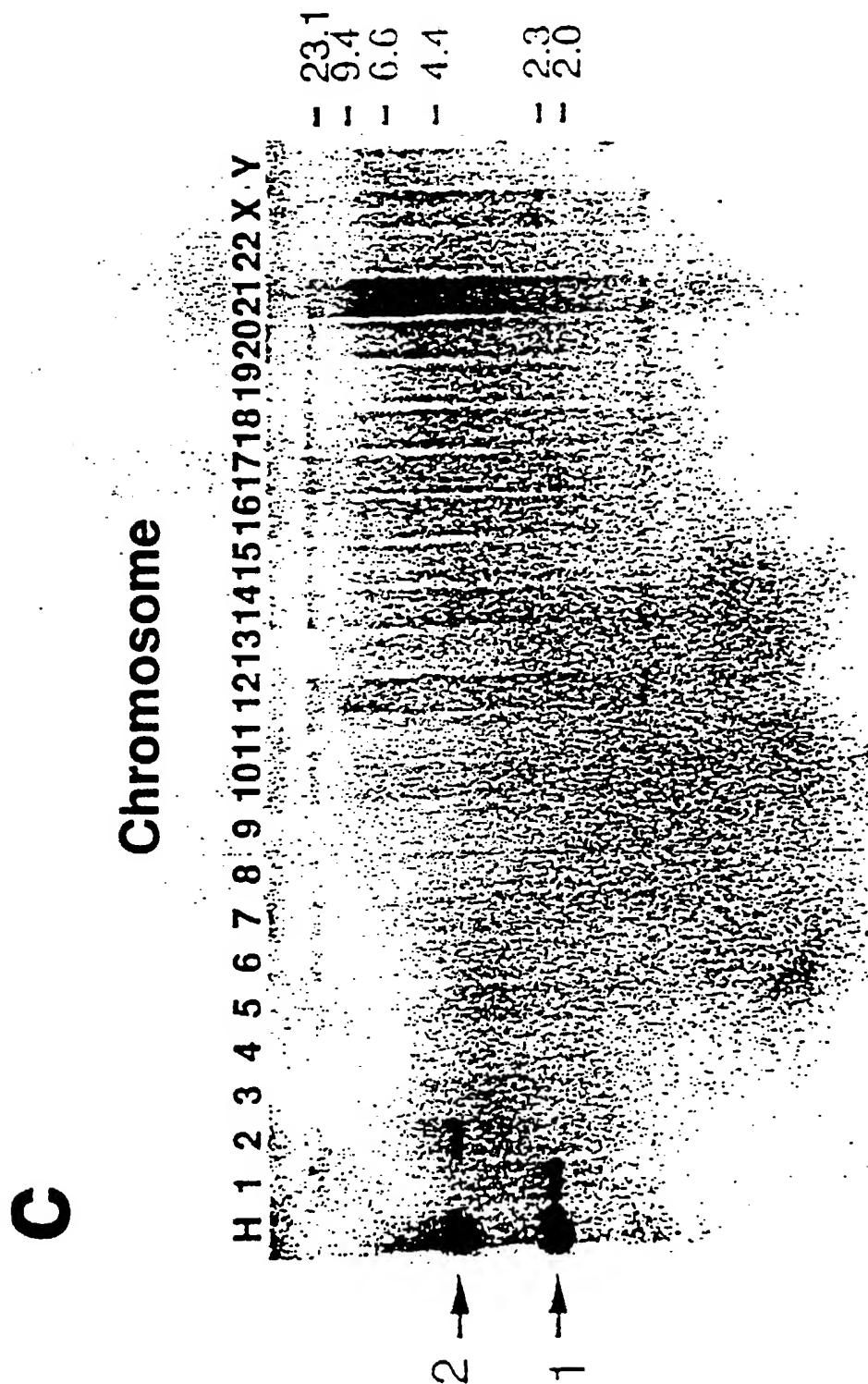


Fig. 19

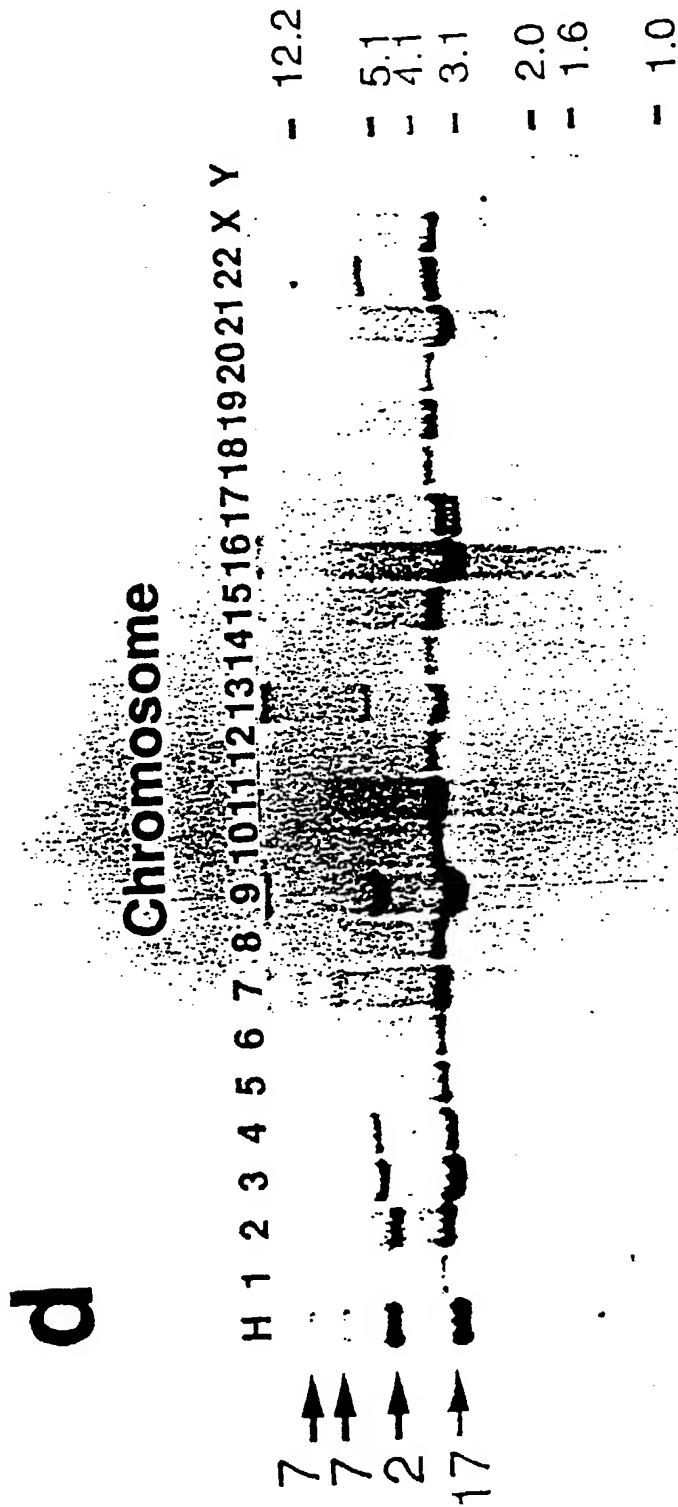


Fig. 20

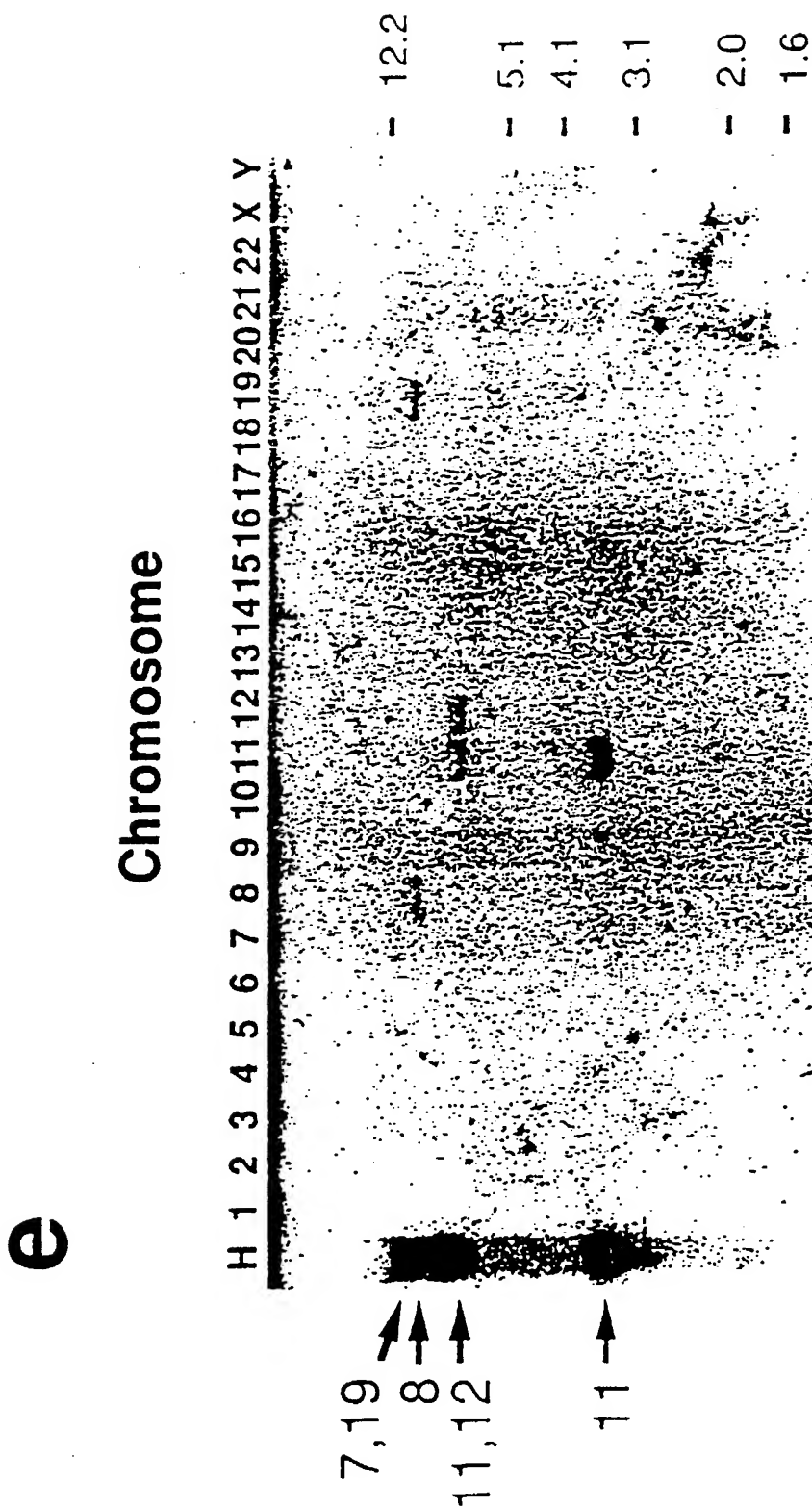


Fig. 21

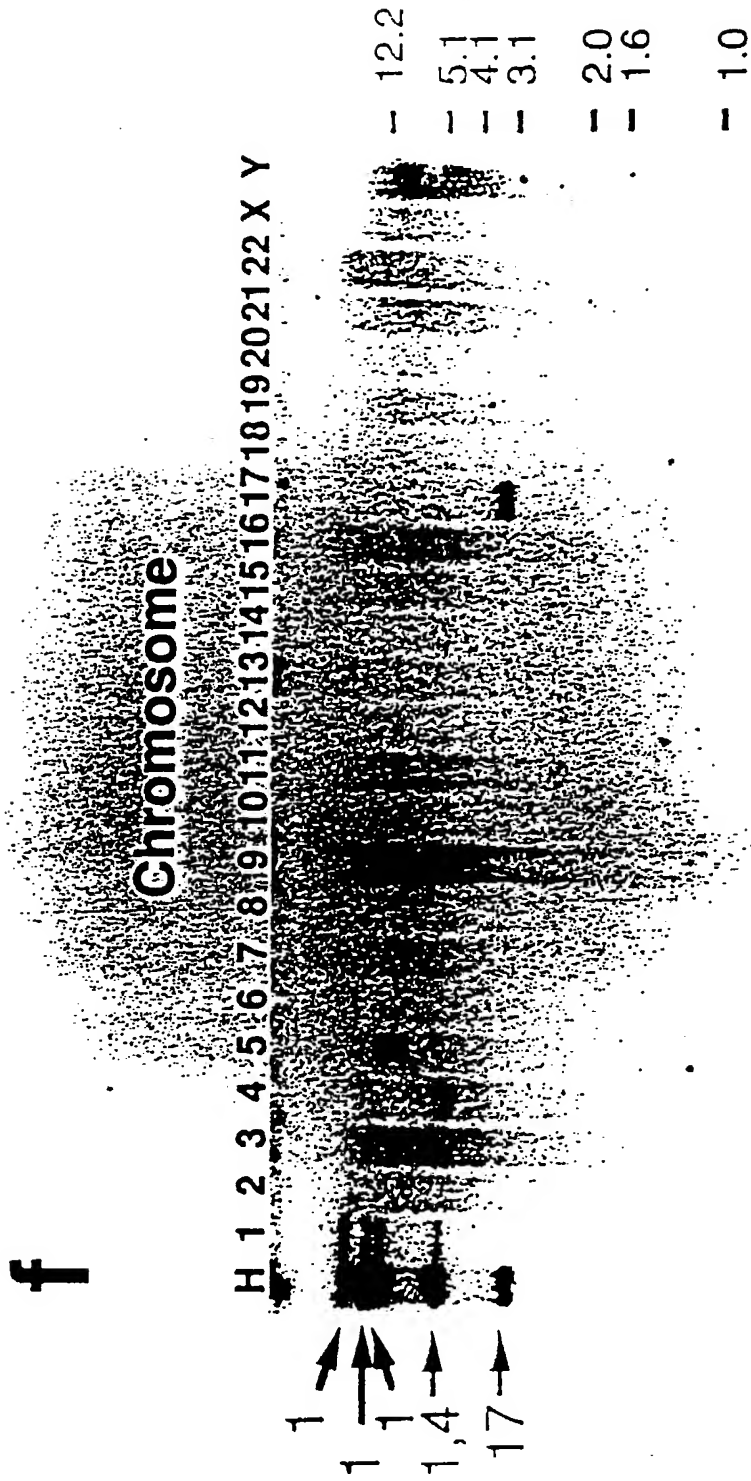


Fig. 22

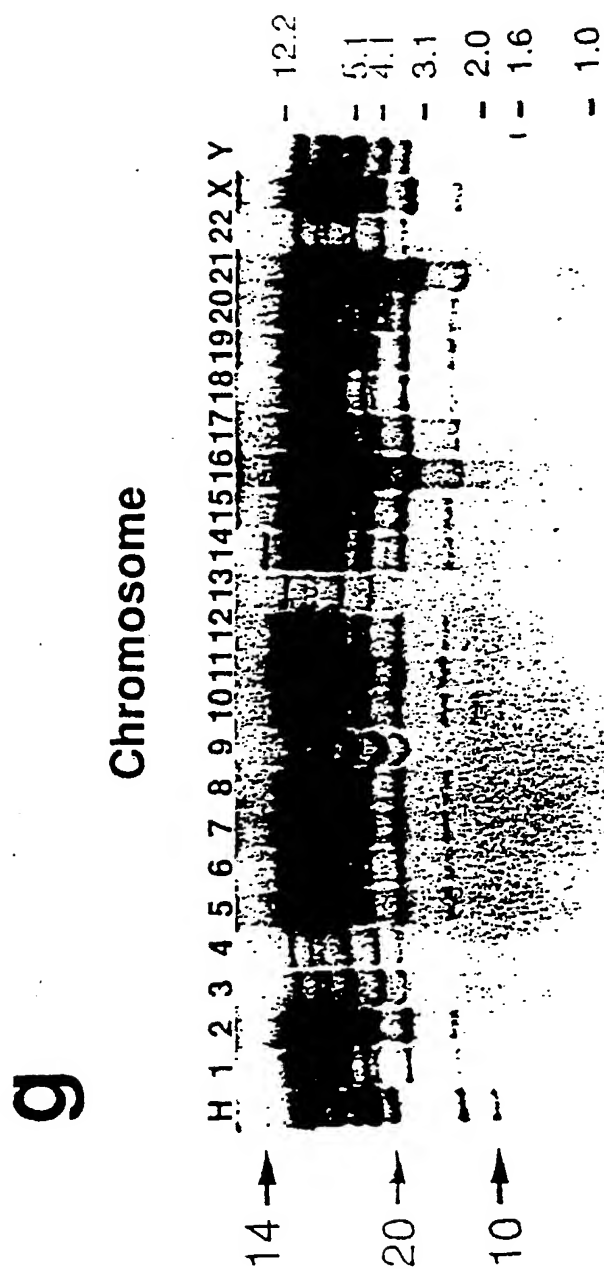


Fig. 23

Chromosomal mapping of each GS by Southern blot technique

Numbers of bands detected with human whole chromosomes				Chromosomes assigned		Background			
Clone	Sequence length	±	±/3 ₁	±/3 ₂	±/3 ₃	Mouse	Chinese hamster		
Single band group:									
c12a11	GS000073	432	1	1	1	1	9	0	0
c12a06	GS000062	540	1	1	1	1	6.15	0	0
c12g01	GS000290	212	1	1	1	1	2	1	1
c13a05	GS000117	359	1	1	1	1	11-	0	0
c13a07	GS000120	355	1	1	1	1	2	0	0
c13f10	GS000206	257	1	1	1	1	14	0	0
c13h01	GS000279	133	1	1	1	1	13-	0	0
c13h02	GS000222	167	1	1	1	1	6	0	0
d0g02	GS000095	397	1	1	1	1	3	0	0
d0h07	GS000154	313	1	1	1	1	11	1	1
d1b10	GS000343	153	1	1	1	1	20	0	0
hm01a12	GS000223	246	1	1	1	1	27	0	0
hm01c09	GS000423	157	0	1	1	1	1	0	0
hm01c12	junk	394	1	1	1	1	17	0	0
hm01f05	GS000066	454	1	1	1	1	19.22	0	0
hm01f10	GS000299	173	0	1	1	1	10	0	0
hm01g09	GS000053	477	1	1	1	1	6	0	0
hm01h07	GS000115	363	1	1	1	1	12	0	0
hm02a02	GS000130	344	1	1	1	1	4	0	0
hm02a04	GS000329	164	1	1	0	0	10	0	0
hm02a01	GS000203	271	1	1	1	1	15	0	0
hm02a01	GS000013	590	1	1	1	1	20	0	0
hm02a02	GS000342	156	0	1	1	1	14	0	0
hm02a05	GS000401	223	1	1	0	0	n.d.	0	0
hm02g02	GS000191	273	1	1	1	1	17	0	0
hm05a05	GS000251	219	1	1	1	1	6	2	0
hm05a10	junk	392	1	1	1	1	1	1	1
hm05c10	GS000009	606	1	1	1	1	1	0	0
km201	junk	169	1	1	1	0	n.d.	0	0
s105	GS000001	703	1	1	1	1	5	0	0
s110	GS000057	471	1	1	1	1	3	0	0
s11d11	GS000307	#175	0	0	0	1	7	0	0
s11h01	GS000259	204	1	1	1	1	3	0	0
s147	GS000060	461	1	1	1	0	2	0	0
s14c06	junk	639	1	1	1	1	1	0	0
s14g02	GS000152	322	1	1	1	1	4	0	0
s14h12	GS000271	193	1	1	1	1	4	1	1
s150	GS000143	330	1	1	1	1	17	0	0
s156	GS000002	306	1	1	1	1	2	1	1
s15b11	GS000250	221	1	1	1	1	14	0	0
s179	GS000275	196	1	1	1	1	n.d.	0	0
s246	GS000234	241	1	1	1	1	9	0	0
s247	GS000247	153	1	1	1	1	1	0	0
s270	junk	135	1	1	1	1	19	0	0

Fig. 24

Numbers of bands detected with human whole chromosomes				Chromosomes assigned		Background			
Clone	Sequence length	±	2/3±	3/3±	3±/3±	Mouse	Chinese hamster		
s306	GS000256	203	1	1	0	1	X	0	0
s309	GS000171	303	1	1	0	1	1	0	0
s342	GS000323	163	1	1	1	1	4	3	2
s331	GS000255	207	1	1	0	1	6,13	1	1
s334	GS000165	312	1	1	1	1	1	0	0
s337	GS000276	193	1	1	1	1	17	0	0
s339	GS000295	130	1	1	1	1	a.d.	0	1
s443	GS000330	231	1	1	1	1	a.d.	0	0
s470	junk	251	1	1	1	1	17	0	0
s474	GS000192	273	1	1	1	1	3	0	0
s503	junk	312	1	1	1	1	12	0	0
s507	junk	600	1	1	1	1	1	2	1
s517	GS000334	161	1	1	1	1	14	1	1
s632	junk	337	1	1	1	1	2	0	0
s633	GS000186	311	1	1	1	1	22	2	1
s530	GS000041	644	1	1	1	1	12	1	1
tw1-04	GS000025	337	1	1	1	1	3,7	0	0
tw1-19	GS000213	253	1	1	1	1	17	0	0
tw1-32	junk	230	1	1	1	1	5	0	0
tw1-37	GS000237	233	1	1	1	1	22	0	0
tw1-42	junk	391	1	1	1	1	8	1	1
tw1-43	GS000093	173	1	1	1	1	14	0	0
tw1-96	GS000133	339	1	1	1	1	11	0	0
Two band group :									
c12f12	GS000195	277	1	2	2	2	1,	1	1
c13d02	GS000042	303	2	2	1	1	2,	0	0
hm01a06	GS000129	344	2	2	2	2	11,13	3	3
hm01a07	GS000207	269	2	2	2	2	7,	0	0
hm01d03	GS000232	243	2	2	2	1	2,	0	0
hm01e01	GS000131	292	2	2	2	2	1,2	0	0
hm02a08	GS000435	302	2	2	2	2	3,	1	1
hm02c04	GS000221	233	2	2	2	2	3,	0	0
hm02c05	GS000146	332	2	2	2	2	17,19,22	0	0
hm03f07	GS000043	303	1	1	2	1	3,	0	0
s11d06	GS000263	203	2	2	2	2	11,12	0	0
s11g12	GS000337	233	2	2	2	2	6,	0	0
s124	GS000083	404	2	2	2	2	9,	1	1
s144	GS000132	342	1	2	2	2	1,7	0	0
s14f03	GS000239	243	1	2	2	2	2,	3	2
s13e02	junk	419	2	2	1	2	6,	0	0
s16b09	junk	420	1	1	1	2	10,14	0	0
s17c09	GS000243	223	2	2	2	2	14,	0	0
s231	junk	284	2	2	2	2	11,	0	0
s234	GS000124	333	2	2	2	2	1,	3	1
s235	GS000235	219	2	2	2	2	11,	0	0
s272	junk	193	2	2	2	2	10,16	1	1

Fig. 25

Numbers of bands detected with human whole chromosomes				Chromosomes assigned				Background	
Clone	Sequence length	E	E/B ₁	E/B ₂	B ₁ /B ₂			Mouse	Chinese hamster
s311	CS000092	333	1	1	2	2	16.	1	1
s313	junk	132	2	2	1	0	20.	0	0
s317	CS000100	339	0	0	1	2	14,14	1	1
s336	CS000134	337	2	2	2	2	12,14	0	0
s333	CS000139	233	2	2	2	1	22,X	0	0
s339	CS000233	137	2	1	1	2	17.	0	0
s394	CS000063	429	2	1	2	2	13,14	0	0
s396	junk	277	2	2	2	2	17.	0	1
s433	junk	452	1	2	2	1	4.	0	0
s436	CS000236	132	2	2	2	2	8,10	1	2
s463	CS000201	274	1	1	2	2	6,15	0	0
s613	junk	250	1	1	1	2	9,13	0	0
s639	CS000257	203	1	2	2	2	2,X	0	0
s656	CS000025	#590	2	2	0	2	6,11	0	0
tw1-33	junk	352	2	2	2	2	1.	0	0
tw1-39	CS000133	#321	2	2	2	2	17.	0	0
tw1-70	CS000061	441	1	1	2	1	11.	0	0
tw1-80	junk	453	2	2	1	2	9,17	2	2
tw1-87	CS000132	316	2	2	2	2	7.	0	0
Three band group									
d0h06	CS000030	417	3	3	3	1	1.	0	0
hm05b07	junk	386	2	3	3	3	5.	0	0
hm05g02	CS000209	267	2	2	2	1	3,17,19	1	1
s129	CS000107	373	3	3	3	3	n.d.	1	1
s173	CS000357	146	1	2	2	3	2.	0	0
s17a10	CS000294	131	3	3	3	3	2,13,22	1	1
s308	CS000412	638	2	2	2	3	XX	1	1
s401	CS000224	249	2	3	3	3	6,6.	0	0
s654	CS000043	491	3	3	3	3	1,22.	0	0
tw1-82	CS000208	267	3	3	3	3	13.	4	0
Four band group									
cl2g07	CS000154	320	4	4	2	3	5, 14.	0	0
cl3a08	CS000055	508	3	3	4	4	2,7,7,17	1	2
cl3c04	CS000108	#376	4	3	3	3	n.d.	0	2
cl3c09	CS000302	193	4	2	4	4	2,17.	7	2
s136	CS000160	313	4	4	4	4	4,X.	2	1
s163	CS000004	#613	4	4	4	2	4,4,8,20	3	1
s479	CS000130	293	4	4	2	2	7,8,11,11,12,19	0	0
Group with 5 or more bands									
cl2r08	CS000253	217	5	5	5	2	2,7,9,14.	2	0
hc01	junk	374	12	12	13	13	1,2,6.	22	20
hd10	junk	361	4	4	4	8	n.d.	12	6
he10	junk	173	6	2	3	3	6,3,9,19,21.	3	3
hm01c05	CS000305	176	9	7	5	5	X	9	8
hm01f04	CS000246	213	8	10	5	5	n.d.	12	12
hm01g02	junk	411	9	6	6	4	10,14,20.	14	6

Fig. 26

Numbers of bands detected with human whole chromosomes					Chromosomes assigned		Background		
Clone	Sequence length	E	E/3 ₁	E/3 ₂	3 ₁ /3 ₂		Mouse	Chinese hamster	
hm02f09	GS000273	442	3	7	7	5	3,3,6,11,13,14,15,16	0	0
hm05a02	GS000096	373	5	6	4	6	2,3,17.	3	3
hm05a04	GS000238	#239	6	6	6	7	n.d.	8	5
km501	junk	350	3	5	5	5	13.	14	7
s11f06	GS000315	170	6	6	6	4	1,2,2,3,4,6,13,15.	0	3
s14f01	GS000407	252	12	11	10	9	1,5,9,13.	6	3
s173	GS000094	337	5	4	6	3	1,1,1,1,4,17	0	0
s255	GS000223	167	10	12	11	14	18.	9	5
s341	junk	494	9	9	3	6	n.d.	15	3
s406	GS000113	364	6	7	5	4	2,7,8,13,20,20	4	1
tw1-46	junk	593	9	10	10	10	1,1,2,2,5,11,X.	3	5
tw1-63	junk	203	3	10	10	12	3,4.	17	11
Bands no detected:									
cl3g02	GS000340	157	0	0	0	0	-	-	-
hm01e10	junk	252	0	0	0	0	-	-	-
hm02d11	GS000274	196	0	0	0	0	-	-	-
s323	GS000273	194	0	0	0	0	-	-	-
s359	GS000199	279	0	0	0	0	-	-	-
s511	junk	233	0	0	0	0	-	-	-
s645	GS000012	#734	0	0	0	0	-	-	-
s647	GS000195	360	0	0	0	0	-	-	-
s651	junk	540	0	0	0	0	-	-	-

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP94/01916

A. CLASSIFICATION OF SUBJECT MATTER		
Int. Cl ⁶ C12N15/11, C12Q1/68//G01N33/566		
According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED		
Minimum documentation searched (classification system followed by classification symbols)		
Int. Cl ⁶ C12N15/11, C12Q1/68//G01N33/566		
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched		
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)		
BIOSIS PREVIEWS, CAS ONLINE		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Nucleic Acids. Res., Vol. 15, 1987, Ou, J. H. "Cloning and characterization of a human ribosomal protein gene with enhanced expression in fetal and neoplastic cells" p. 8919-8934	1-6 (164)
X	Differentiations, Vol. 33, 1986, Oshima, R. G. et al. "Comparison of mouse and human keratin 18:A component of intermediate filaments expressed prior to implantation" p. 61-68	1-6 (226)
X	J. Biol. Chem., Vol. 265, 1990, Wilkin, D. J. et al. "Isolation and sequence of the human farnesyl pyrophosphate synthetase cDNA:coordinate regulation of the mRNAs for farnesyl pyrophosphate synthetase, 3-hydroxy-3-methylglutaryl coenzyme A reductase, and 3-hydroxy-3-methylglutaryl coenzyme A synthetase" p. 4607-4614	1-6 (255)
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.		
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Date of the actual completion of the international search		Date of mailing of the international search report
February 6, 1995 (06. 02. 95)		March 7, 1995 (07. 03. 95)
Name and mailing address of the ISA/ Japanese Patent Office		Authorized officer
Facsimile No.		Telephone No.

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International application No.

PCT/JP94/01916

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biol. Chem., Vol. 266, 1991, Batra, S. K. et al. "Molecular cloning and sequence analysis of the human ribosomal protein S16" p. 6830-6833	1-6 (275)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 87, 1990, Ben-Ishai, R. et al. "A human cellular-sequence implicated in trk oncogene activation is DNA damage inducible" p. 6039-6043	1-6 (313)
X	J. Biol. Chem., Vol. 263, 1988, Fischer, R. et al. "Multiple divergent mRNAs code for a single human calmodulin" p. 17055-17062	1-6 (386)
X	J. Cell Biol., Vol. 108, 1989, Barnett, T. R. et al. "Carcinoembryonic antigens: Alternative splicing accounts for the multiple mRNAs that code for novel members of the carcinoembryonic antigen family" p. 267-276	1-6 (446)
X	J. Biol. Chem., Vol. 265, 1990, Natsumeda, Y. et al. "Two distinct cDNAs for human IMP dehydrogenase" p. 5292-5295	1-6 (454)
X	Genes Dev., Vol. 7, 1993, Patton, J. G. et al. "Cloning and characterization of PSF a novel pre-mRNA splicing factor" p. 393-406	1-6 (706)
X	Nucleic Acids Res., Vol. 16, 1988, Stanford, D. R. et al. "The complete primary structure of the human snRNP E protein" p. 10593-10605	1-6 (711)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 84, 1987, Inoue, C. et al. "Evolutionary conservation of the insulinoma gene rig and its possible function" p. 6659-6662	1-6 (723)
X	J. Immunol., Vol. 144, 1990, Jongstra-Bilen, J. et al. "Human and mouse LSP1 genes code for highly conserved phosphoproteins" p. 1104-1110	1-6 (741)
X	Biochem. J., Vol. 248, 1987, Sakai, I. et al. "The cDNA and protein sequences of human lactate dehydrogenase-B" p. 933-936	1-6 (772)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP94/01916

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Biochim. Biophys. Acta., Vol. 1089, 1991, Tamura, T. et al. "Molecular cloning and sequence analysis of cDNAs for five major subunits of human proteasomes (multicatalytic proteinase complexes)" p. 95-102	1-6 (775)
X	Mol. Cell. Biol., Vol. 3, 1983, Cowan, N. J. et al. "Expression of human alpha-tubulin genes: interspecies conservation of 3' untranslated regions" p. 1738-1745	1-6 (820)
X	Nucleic Acids Res., Vol. 17, 1989, Taaman, J. W. et al. "Nucleotide sequence of cDNA encoding subunit Vlb of human cytochrome c oxidase" p. 1766-1766	1-6 (844)
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